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Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
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                                                                                                                                                                                                                                    Result
                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                 pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                and is derived by analysis of the total score distribution
                                                                                                                                                                                                                  Score
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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                                                                                                                   AAW04339
AAW04340
AAB71918
AAY70890
  AAY70901
                                         AAY70899
                                                            AAY70925
                                                                                  AAY70902
                                                                                                   AAY70913
                                                                                                                                                                                                                                                                                 SUMMARIES
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                                                            ATP diphosphohydro
ATP diphosphohydro
ATP diphosphohydro
Soluble human CD39
Protein encoded by
Human soluble CD39
Protein encoded by
Human soluble CD39
                                                                                                                                                                                                                    Description
      Human soluble CD39 
Protein encoded by
                                               Protein encoded by
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| 110 110 110 110 110 110 110 110 110 110 | 11 12 13 14 15 |
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| 4 4 5 4 5 4 6 5 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 | 75 75 75 75 |
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| AAY70912 AAY70891 AAY70914 AAY70921 AAW04264 AAW04264 AAW04264 AAW70910 AAB71917 AAY70910 AAB71917 AAY44850 AAW744850 AAW744869 AAY44850 AAW72239 AAY44850 AAW72239 AAW742643 AAW72239 AAW742643 AAW742643 AAW742643 AAW742643 AAW742643 AAW742643 AAW742643 AAW742643 AAW742643 AAW74818 | AAY70924 AAY70900 AAY70923 AAY70888 AAY70889 AAY70889 |
| Human CD39-L4-2/3 Protein encoded by Human soluble CD39 Human CD39-L66 pro Human CD39-L4 vari Human CD39-L4 vari Human CD39-L4 vari Human CD39-L1ke pr Human CD39-L1ke prote Human CD39-L1ke prote Human CD39-L1ke prote Human CD39-L1ke ge | |

ALIGNMENTS

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AAW04339
ID AAW0
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PF PT PT PT
                                                                                                                                                                 W09632471-A2
                                                                                                                                                                                                        platelet aggregation; thrombogenicity; anti-haemostatic.
                                                                                                                                                                                                                    ATP diphosphohydrolase; ATPDase; bovine aorta; pig pancreas; apyrase; CD39; lymphoid cell activation antigen; enzyme;
                                                                                                                                                                                                                                                   ATP diphosphohydrolase fragment from pig pancreas.
                                                                                                                                                                                                                                                                         29-DEC-1996 (first entry)
                                                                                                                                                                                                                                                                                              AAW04339;
                                                                                                                                                                                                                                                                                                                 AAW04339 standard; Protein; 20
                                                                                                                         10-APR-1996;
                                                             Beaudoin AR, Sevigny J;
                                                                               (UYSH ) UNIV SHERBROOKE.
                                                                                                   10-APR-1995;
                                                                                                                                                                                     Sus scrofa
                                                                                                                                              17-OCT-1996
                                                                                                    95US-0419204
                                                                                                                          96WO-CA00223
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thrombogenicity

WPI; 1996-477122/47.

Isolated ATP di:phospho:hydrolase enzymes - have anti-haemostatic

activity, useful for reducing platelet aggregation and

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AAW04340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                  Pancreatic (AAW0433) ATPDases have been partially sequenced. The sequences have been found to be highly homologous to a human lymphoid cell activation antigen designated CD39 (Maliszenski et at. (1994). J. Immunol: 3574-3583). The complete sequences of t ATPDases types I and II have not been obtained yet. Assuming that the CD39 gene product is an ATPDase type II. the use of CD39 in the reduction of platelet aggregation and of thrombogenicity may be contemplated, as well as a process of making ATPDases using the CD39 sequence (AAT38516).
Sequence
                                                                                                                                                               The bovine aorta (AAW04335 to AAW04338 and AAW04340) and porcine
                                                                                                                                                                                                   Claim 2; Page 47; 60pp; English.
                                                                                                                                                                                                                                                          Isolated ATP di:phospho:hydrolase enzymes - have anti-haemostatic
                                                                                                                                                                                                                                      thrombogenicity
                                                                                                                                                                                                                                                                                                    WPI; 1996-477122/47.
                                                                                                                                                                                                                                                                                                                                                                                               10-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                            10-APR-1996;
                                                                                                                                                                                                                                                                                                                                 Beaudoin AR,
                                                                                                                                                                                                                                                                                                                                                              (UYSH ) UNIV SHERBROOKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-OCT-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09632471-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              platelet aggregation; thrombogenicity; anti-haemostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP diphosphohydrolase; ATPDase; bovine aorta; piq pancreas; apyrase; CD39; lymphoid cell activation antigen; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP diphosphohydrolase fragment (5) from bovine aorta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-DEC-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at. [1994). J. Immunol.: 3574-3583). The complete sequences of the ATPDases types I and II have not been obtained yet. Assuming that the CD39 gene product is an ATPDase type II, the use of CD39 in the reduction of platelet aggregation and of thrombogenicity may be contemplated, as well as represented in the machine as well as a specific process of making ATPDases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW04340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW04340 standard; Protein; 16 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  using the CD39 sequence (AAT38516).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 46; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pancreatic (AAW04339) ATPDases have been partially sequenced. The sequences have been found to be highly homologous to a hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The bovine aorta (AAW04335 to AAW04338 and AAW04340) and porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ymphoid
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                                                                                                                                                                                                                                         useful for reducing platelet aggregation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell activation antigen designated CD39 (Maliszenski et types I and IT here.
 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                              Sevigny J;
                                                                                                                                                                                                                                                                                                                                                                                           95US-0419204.
                                                                                                                                                                                                                                                                                                                                                                                                                          96WO-CA00223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 96; DB L/; 100.0%; Pred. No. 5.8e-10; or Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 20;
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                                                                        Matches
                                                                                                     Query Match
                                                                                          Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                   active fragment may be administered to treat or prevent stroke in a subject susceptible to intracranial haemorrhaging or an ischaemic disorder. The CD39 polypeptide inhibits ADP-mediated platelet aggregation or leukocyte accumulation and/or ATP by increasing ADP catabolism to the subject. CD39 or its active fragment is useful for treating or preventing vascular disorder, pulmonary embolus, venous thrombosts, myocardial infarction, transient ischaemic attack, unstable angina, reversible ischaemic neurological deficit and sickle cell andemia. It is also useful for treating or preventing a stroke disorder in a subject undergoing heart surgery, lung surgery, spinal surgery, brain surgery, vascular surgery, abdominal surgery, or organ transplantation surgery.
                                                                                                                                    Sequence
165 ETNNQETFGALDLGGASTQ 183
                                                                                                                                                                                                                                                                                                                                                              The present sequence is the active fragment of human CD39. CD39 or its
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 14; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating stroke in a subject susceptible to intracranial hemorrhaging and an ischemic disorder, involves administering a CD39 polypeptide which inhibits ADP-mediated platelet aggregation or leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                            accumulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pinsky DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-202805/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-AUG-2000; 2000WO-US22060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200111949-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMO sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stroke; thrombotic disorder; ischaemic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; CD39; vasotropic; cerebroprotective; haemostatic; thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Soluble human CD39 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB71918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB71918 standard; Protein; 439 AA.
                                                                                    Local Similarity
                                 1 KSDTQETYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KSDTQETYGALDLGGA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KSDTQETYGALDLGGA 16
                                                                      14;
                                                                                                                                      439 AA;
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0374586
                                                                             78.1%; Score 75; DB 22; 73.7%; Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.4%; Score 82;
100.0%; Pred. No.
                                                                  4;

 Mismatches

                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.3e-07;
                                                                                            Length 439;
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                                                              Indels
                                                           0;
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                                                           Gaps
                                                           0;
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RESULT 4 AAY70890

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unstable angina; myocardial infarction; stroke; coronary artery disease atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; lung ischaemia; thrombolytic; cerebral ischaemia; thrombotic disorder; coronary artery thrombosis; cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis; norm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein encoded by fusion construct of human soluble CD39 cDNA-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVF; PE; pulmonary embolism; transient ischaemic attack; thrombus formation; occlusion; reocclusion; stenosis; restenosis; antianginal; cardiant; cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant; correst of the control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soluble CD39; ADP-induced platelet activation; platelet aggregation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY70890;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200023094-A2.
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                                                                                                                                                                                                                                                       myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, platelet-associated ischaemic disorder including lung ischaemia, coronary ischaemia and cerebral ischaemia, thrombotic disorder including coronary
                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the protein enocoded by a fusion construct of sol(soluble)CD39 having apyrase activity. Fusion of 12 amino acids from the N-terminus of mature human ILZ to the solCD39 coding region results in high levels of both expression and activity in the supernatants of transfected cells. This is used in the treatment of unstable angina, in the supernatants of transfected cells. This is used in the treatment of unstable angina, the supernatants of the supernatants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting platelet activation and recruitment, useful for treating a mammal suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, comprises administering soluble CD39 polypeptides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAD00201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maliszewski CR, Gayle RB, Marcus AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IMMV ) IMMUNEX CORP.
(CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-OCT-1999;
                                                                                             artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis, thrombosis, peripheral artery thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Page 95-97; 118pp; English.
                                                                restenosis of blood vessels or stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-339518/29.
          454 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0104585.
98US-0107466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US23641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0149010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "N-terminal region" 16..454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label- Mature_human_interleukin_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Human soluble CD39 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coronary artery disease
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Sequence

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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coagulopathy, deep venous thrombosis; DVT; pulmonary embolism; PE; thrombus formation; occlusion; stenosis; restenosis; angiogenesis; antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet associated ischaemic disorder; thrombotic disorder; reocclusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY70913 standard; Protein; 454 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human soluble CD39 and IL2 N-terminus comprising fusion construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cardiant; vasotropic; thrombolytic; inhibitor; interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soluble CD39; solCD39; human; apyrase activity; platelet activation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY70913;
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The present sequence is a fusion construct, comprising the N-terminal amino acids of mature human interleukin2 (IL2) and soluble CD39 (solCD39) amino acids of mature human interleukin2 (IL2) and soluble CD39 (solCD39) region, that has apyrase activity, This results in high levels of solCD39 expression and activity in the transfected cells. Soluble CD39 is solCD39 expression and activity in the transfected cells. Soluble CD39 is retains the capacity to metabolise ATP and ADP at relevant concentrations retains the capacity to metabolise ATP and ADP at relevant concentrations and the ability to block and reverse ADP-induced platelet activation and recruitment, including platelet aggregation. Soluble CD39 polypeptides are useful for inhibiting anglogenesis. It is useful for the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, precedency and the approach of the coronary artery precedency and the contraction of the coronary artery precedency and the coronary artery precedency are coronary artery precedency and the coronary artery precedency are coronary artery precedency and the coronary artery precedency and the coronary artery precedency are coronary artery precedency and the coronary artery precedency are coronary artery precedency and the coronary artery precedency are coronary artery precedency and the coronary artery precedency are coronary artery precedency and the coronary artery precedency are coronary are cor
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06-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200023459-A1.
                                                                                                                                                                                                                                                                                                                                      Claim 6a; Page 95-97; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                      New soluble CD39 polypeptides having apyrase activity, useful for inhibiting angiogenesis and treating unstable angina, myocardial infarction, stroke, coronary artery disease or injury .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maliszewski CR, Gayle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000-339644/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0149010
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98US-0107466
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16..454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Human soluble CD39 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Mature_human_interleukin_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.1%;
73.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "N-terminal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RВ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.
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Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Price VL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21; Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gimpel SD;
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Inhibiting platelet activation and recruitment, useful for treating a mammal suffering from unstable angina, myocardial infarction, stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                     WPI; 2000-339518/29.
                                                                              Maliszewski CR, Gayle RB,
                                                                                                        (IMMV ) IMMUNEX CORP.
                                                                                                                                                       13-AUG-1999;
                                                                                                                                                                                                                                                                  WO200023094-A2.
                                                                                                                                                                                 16-OCT-1998;
                                                                                                                                                                                                           13-OCT-1999;
                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                               Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; lung ischaemia; thrombolytic; cerebral ischaemia; thrombotic disorder; coronary artery thrombosis; cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
                                                                                                                                                                                                                                                                                                                                                                   Reg 1on
                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coronary ischaemia; vascular occlusion; IgkappaLsolCD39 construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT, PE; pulmonary embolism; transient ischaemic attack; thrombus formation; occlusion; reocclusion; stenosis; restenosis; antianginal; cardiant; cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soluble CD39; ADP-induced platelet activation; platelet aggregation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein encoded by IgkappaLsolCD39 construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMO sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY70902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY70902 standard; Protein; 463 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         venous thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood vessels or stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 ETNNQETFGALDLGGASTQ 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coronary,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KSDTQETYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coronary and cerebral ischaemia, thrombotic disorders including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peripheral and cerebral artery thrombosis, intracardiac and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              454 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                   99US-0149010.
                                                                                                                                                                  98US-0107466
                                                                                                                                                                              98US-0104585
                                                                                                                                                                                                          99WO-US23641
                                                                                                                                                                                                                                                                                                                                      /note= "Derived from IL-2"
25..32
                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                    /note= "Igkappa leader sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.18;
73.78;
                                                                                                                                                                                                                                                                                                                  "Derived from solCD39"
                                                                                                                                                                                                                                                                                     "Soluble portion of CD39"
                                                                              Marcus AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 75; DB 21;
Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
  06-NOV-1998;
                                                         13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                          atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE; thrombus formation; occlusion; stenosis; restenosis; anglogenesis; antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant; cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2; Ig;
                       16-0CT-1998;
                                                                                             27-APR-2000.
                                                                                                                                   WO200023459-Al.
                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                       Cleavage-site
                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soluble CD39; solCD39; human; apyrase activity; platelet activation; unstable angina; myocardial infarction; stroke; coronary artery disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human soluble CD39 fusion protein construct, IgkappaLsolCD39.
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY70925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY70925 standard; Protein; 463 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the protein encoded by IgkappaLsolCD39 construct. This is used for transfent expression of soluble(sol)CD39 in recombinant cells for determining enzymatic activity and platelet inhibitory activity and platelet inhibitory activity and platelet inhibitory activity angina, myocardial infarction, stroke, coronary artery disease or injury, platelet-associated ischaemic disorder including lung ischaemia, coronary ischaemia and cerebral ischaemia, thrombotic disorder including coronary artery thrombosic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 ETNNQETFGALDLGGASTQ 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            restenosis of blood vessels or stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6; Page 116-118; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coronary artery disease or injury, comprises administering soluble CD39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KSDTQETYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          463 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
98US-0107466
                   98US-0104585
                                                     99WO-US22955.
                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                       /note=
                                                                                                                                                                                               /note= "Residues derived from human interleukin 2 (IL2)"
                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                         /note= "Derived from human immunoglobulin Ig kappa"
                                                                                                                                                                                                                                                                                                  /label= Leader_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.1%; Score 75; DB 21; 73.7%; Pred. No. 0.00012;
                                                                                                                                                                                                                                     "Cleavage site of leader sequence"
                                                                                                                                                               "Human soluble CD39 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21; Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myocardial infarction, coronary artery disease or injury embolism, atherosclerosis, peripheral vascular occlusion, preeclampsia, platelet-associated ischaemic disorders including lung, coronary and cerebral ischaemia, thrombotic disorders including coronary, peripheral and ischaemia thrombosis, intracardiac and venous thrombosis, cerebral artery thrombosis, intracardiac and venous thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and translent ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or thrombus formation or reformation, occlusion, reocclusion, stenosis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the fusion protein construct, 1gkappaLsolCD39. This construct comprises of the leader peptide from human immunoglobulin 1g kappa, linked to the soluble CD39 (solCD39) protein region by few residues derived from human interleukin 2 (hIL2). SolCD39 has apyrase activity and is constructed by removing the N- and C-terminal transmembrane domains. It retains the capacity to metabolise ATP and ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 116-118; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New soluble CD39 polypeptides having apyrase activity, useful for inhibiting angiogenesis and treating unstable angina, myocardial infarction, stroke, coronary artery disease or injury \dot{}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-339644/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at relevant concentrations and the ability to block and reverse at relevant concentrations and the recruitment, including platelet Apprinduced platelet activation and recruitment, including platelet aggregation. Soluble CD39 polypeptides are useful for inhibiting anglogenesis. It is useful for the treatment of unstable angina, straining the property of the presentation of the property of the pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maliszewski CR, Gayle RB, Price VL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                          peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT; PE; pulmonary embolism; transient ischaemic attack; thrombus formation; occlusion; reocclusion; stenosis; restenosis; antianginal; cardiant; cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant; coronary ischaemia; vascular occlusion; pIL2Triml variant.
                                                                                                                                                                                                                                                                                                                                                                                                                    Soluble CD39; ADP-induced platelet activation; platelet aggregation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; lung ischaemia; thrombolytic; cerebral ischaemia; thrombotic disorder; coronary artery thrombosis; cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis; num.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein encoded by Trim 1 construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY70899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY70899 standard; Protein; 464 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   restenosis of blood vessels or stroke.
       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 ETNNQETFGALDLGGASTQ 207
                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KSDTQETYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocal Similarity
                                  .eavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         463 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0149010.
Location/Qualifiers 24..25 26..464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.1%;
73.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 75; DB 21;
Pred. No. 0.00012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gimpel SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21; Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IgkappaLsolCD39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vascular occlusion, preeclampsia, embolism, platelet-associated isohaen disorder including lung ischaemia, coronary ischaemia and cerebral ischaemia, a thrombotic disorder including coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, thrombosis, coagulapathy, deep venous thrombosis, thrombosis, coagulapathy, deep venous thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack. Soluble (DJ9 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the protein encoded by Triml construct. pIL2Triml variant was constructed by removing the human IL2 residues from solCD39 fusion construct. Fusion of 12 amino acids from the N-terminus of mature human IL2 to the solCD39 coding region results in high levels of both expression and activity in the supernatants of transfected cells. SolCD39 is used in the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral stroke, coronary artery disease or injury, atherosclerosis, peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting platelet activation and recruitment, useful for treating a mammal suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, comprises administering soluble CD39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maliszewski CR, Gayle RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-NOV-1998;
13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200023094-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 11; Page 111-112; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-339518/29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-1998;
                                                                                             Soluble CD39; solCD39; human; apyrase activity; platelet activation; unstable angina; myocardial infarction; stroke; coronary artery diseatherosclerosis; peripheral vascular occlusion; preeclampsia; emboliplatelet associated ischaemic disorder; thrombotic disorder; reocclusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                 coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE; thrombus formation; occlusion; stenosis; restenosis; angiogenesis; anticoagulant; antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
                                                                                                                                                                                                  Human soluble CD39 fusion protein construct, pIL2LTrim1.
                                                                                                                                                                                                                                              17-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                          AAY70922 standard; Protein; 464 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vessels or stroke.
               cardiant; vasotropic; thrombolytic; inhibitor; interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                              190 ETNNQETFGALDLGGASTQ 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KSDTQETYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0107466.
99US-0149010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0104585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US23641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marcus AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 75; DB 21; Length 464; Pred. No. 0.00012;
                                                                                                      clusion; preeclampsia; embolism;
thrombotic disorder; reocclusion;
                                                                                                                                                   coronary artery disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT 10
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                                                                                                                                                                                                                                                                   Matches
Protein encoded by Trim 4 construct.
                                 17-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       and the ability to block and reverse ADP induced platelet activation and recruitment, including platelet aggregation. Soluble CD39 polypeptides are useful for inhibiting anglogenesis. It is useful for the treatment of unstable anglna, stroke, myocardial infarction, coronary artery disease or injury embolism, atherosclerosis, peripheral vascular occlusion, platelet associated ischaemic disorders including lung, coronary and cerebral ischaemia, thrombotic disorders including coronary,
                                                                           AAY70901;
                                                                                                 AAY70901 standard; Protein; 473 AA
                                                                                                                                                                                                                                                                                                                                                            stemosis or restemosis of blood vessels or stroke.
                                                                                                                                                                                                                                                                                                                                                                     peripheral and cerebral artery thrombosis, intracardiac and venous thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion,
                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the fusion protein construct, pIL2LTrim1. This construct comprises of the leader peptide from human interleukin 2 (hIL2) and soluble CD39 (solCD39) protein region, having apyrase activity. The two regions are joined by an intervening Ala residue. Soluble CD39 is constructed by removing the N- and C-terminal transmembrane domains. It retains the capacity to metabolise ATP and ADP at relevant concentrations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New soluble CD39 polypeptides having apyrase activity, useful for inhibiting angiogenesis and treating unstable angina, myocardial infarction, stroke, coronary artery disease or injury -
                                                                                                                                                                                          190 ETNNQETFGALDLGGASTQ 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Page 111-112; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-339644/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-1998;
06-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200023459-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                            1 KSDTQETYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                   464 AA;
                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0149010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0107466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Cleavage site of leader sequence" 26..464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Leader_peptide
/note= "Derived from human interleukin 2 (hIL2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Human soluble CD39 protein"
                                                                                                                                                                                                                                                                       78.1%; Score 75; DB 21; Length 464; 73.7%; Pred. No. 0.00012;
                                                                                                                                                                                                                                                              4
                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                    Indels
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199 ETNNQETFGALDLGGASTQ 217

1 KSDTQETYGALDLGGASTQ 19

Matches Query Match Best Local

Similarity

78.1%; Score 75; DB 21; 73.7%; Pred. No. 0.00012; 4; Mismatches

DB 21; Length 473;

Indels

0;

0,

Conservative

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The present sequence is the protein encoded by Trim4 construct. pIL2Trim4 CC variant was constructed by removing the human IL2 residues from solCD39 CC fusion construct. Fusion of 12 amino acids from the N-terminus of mature CC human IL2 to the solCD39 coding region results in high levels of both CC expression and activity in the supernatants of transfected cells. SolCD39 cis used in the treatment of unstable angina, myocardial infarction, CC vascular occlusion, preeclampsia, embolism, platelet-associated ischaemic CC vascular occlusion, preeclampsia, embolism, platelet-associated ischaemic CC disorder including lung ischaemia, coronary ischaemia and cerebral cC disorder including lung ischaemia, coronary ischaemia and cerebral schaemic, a thrombosis, intracardiac thrombosis, peripheral artery thrombosis, thrombosis, coagulopathy, deep venous collibration composis, coagulopathy, deep venous collibration of reformation. Ordingion resonation thrombosis formation or reformation or reformation or resonation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                          vessels or stroke.
                                               reformation, occlusion, reocclusion, stenosis or restenosis of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                              coronary artery disease or injury, comprises administering soluble CD39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mammal suffering from unstable angina, myocardial infarction, stroke,
                                                                                                                                                                                                                                                                                                                                                                                                        Example 11; Page 114-116; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-339518/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soluble CD39; ADP-induced platelet activation; platelet aggregation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; cursonary artery thromboslytic; cerebral ischaemia; thrombotic disorder; coronary artery thrombosls; cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis; peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT; pE; pulmonary embolism; transient ischaemic attack; thrombus formation; occlusion; recoclusion; stenosis; restenosis; antianginal; cardiant; cerebroprotective; antiarteriosclerotic; vascutopic; anticoagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maliszewski CR, Gayle RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-1998;
06-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L3-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W0200023094-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coronary ischaemia; vascular occlusion; pIL2Trim4 variant
473 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0149010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0104585.
98US-0107466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US23641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 26..27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Soluble portion of CD39"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marcus AJ;
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cc and soluble (D39 (sol(D39) protein region, having apyrase activity.

Cs soluble (D39 (sol(D39) protein region, having apyrase activity.

Cs soluble (D39 is constructed by removing the N- and C-terminal

ctransmembrane domains. It retains the capacity to metabolise ATP and ADP

Cc transmembrane domains. It retains the capacity to block and reverse

ADP-induced platelet activation and recruitment, including platelet

cc aggregation. Soluble (D39 polypeptides are useful for inhibiting

cc anglogenesis. It is useful for the treatment of unstable angina, stroke,

cc myocardial infarction, coronary artery disease or injury, embolism,

cc atherosclerosis, peripheral vascular occlusion, preeclampsia, platelet-

cc associated ischaemic disorders including lung, coronary and cerebral

cc associated irrembotic disorders including coronary, peripheral and

cc cerebral artery thrombosis, intracardiac and venous thrombosis, pripheral attack. Soluble CD39 is also useful for preventing

cc transient ischaemic attack. Soluble CD39 is also useful for preventing

cc restenosis of blood vessels or stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Soluble CD39; solCD39; human; apyrase activity; platelet activation; unstable angina; myocardial infarction; stroke; coronary artery disease; atheroselerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE; thrombus formation; occlusion; stenosis; restenosis; angiogenesis; antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY70924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY70924 standard; Protein; 473 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human soluble CD39 fusion protein construct, pIL2LTrim4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-1998;
06-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200023459-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New soluble CD39 polypeptides having apyrase activity, useful for inhibiting anglogenesis and treating unstable angina, myocardial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-2000
                                                                                                                                                                                                                                                                                                                                                      The present sequence is the fusion protein construct, pIL2LTrim4. This construct comprises of the leader peptide from human interleukin 2 (hIL2)
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 114-116; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maliszewski CR, Gayle RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          infarction, stroke, coronary artery disease or injury -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0149010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US22955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0104585.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Cleavage site of leader sequence"
35..473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Derived from human interleukin 2 (hIL2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Human soluble CD39 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Price VL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gimpel SD;
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Sequence

473 AA;

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RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             platelet-associated ischaemic disorder; lung ischaemia; thrombolytic; cerebral ischaemia; thrombotic disorder; coronary artery thrombosis; cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis; peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT; PE; pulmonary embolism; transient ischaemic attack; thrombus formation; occlusion; reocclusion; stenosis; restenosis; antianginal; cardiant; cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant; coronary ischaemia; vascular occlusion; plizTrim3 variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY70900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY70900 standard; Protein; 474 AA.
The present sequence is the protein encoded by Trim3 construct. pIL2Trim3 variant was constructed by removing the human IL2 residues from solCD39 fusion construct. Fusion of 12 amino acids from the N-terminus of mature human IL2 to the solCD39 coding region results in high levels of both expression and activity in the supernatants of transfected cells. SolCD39 is used in the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, platelet-associated ischaemic disorder including lung ischaemia, coronary ischaemia and cerebral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Soluble CD39; ADP-induced platelet activation; platelet aggregation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein encoded by Trim 3 construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 ETNNQETFGALDLGGASTQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200023094-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                     coronary artery disease or injury, comprises administering soluble CD39
                                                                                                                                                                                                                                                       Inhibiting platelet activation and recruitment, useful for treating mammal suffering from unstable angina, myocardial infarction, stroke
                                                                                                                                                                                                                                                                                                                  WPI; 2000-339518/29.
                                                                                                                                                                                                                                                                                                                                                   Maliszewski CR, Gayle RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                           13-AUG-1999;
                                                                                                                                                                                    Example 11; Page 113~114; 118pp; English.
                                                                                                                                                                                                                       polypeptides .
                                                                                                                                                                                                                                                                                                                                                                                    (CORR ) CORNELL
                                                                                                                                                                                                                                                                                                                                                                                                      (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KSDTQETYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0107466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US23641
                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0149010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0104585.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note=
                                                                                                                                                                                                                                                                                                                                                                                        RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.1%;
73.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Soluble portion of CD39"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 75; DB 21; Pred. No. 0.00012
                                                                                                                                                                                                                                                                                                                                                       Marcus AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21; Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                        stroke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
The present sequence is the fusion protein construct, pIL2LTrim3. This
                             Claim 6; Page 113-114; 122pp; English.
                                                              New soluble CD39 polypeptides having apyrase activity, useful for inhibiting angiogenesis and treating unstable angina, myocardial
                                                   infarction, stroke, coronary artery disease or injury
                                                                                                        WPI; 2000-339644/29.
                                                                                                                                                                                                                                                                                                                                      Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soluble CD39; solCD39; human; apyrase activity; platelet activation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
                                                                                                                            Maliszewski CR, Gayle RB, Price VL,
                                                                                                                                                       (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                           16-OCT-1998;
06-NOV-1998;
                                                                                                                                                                                                                              13-OCT-1999;
                                                                                                                                                                                                                                                                            WO200023459-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombus formation; occlusion; stenosis; restenosis; angiogenesis; antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant; cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human soluble CD39 fusion protein construct, pIL2LTrim3.
                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ischaemia, a thrombotic disorder including coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, intracardiac thrombosis, venous thrombosis, trombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY70923 standard; Protein; 474 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reformation, occlusion, reocclusion, stenosis or restenosis of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vessels or stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 ETNNQETFGALDLGGASTQ 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KSDTQETYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          474 AA;
                                                                                                                                                                             99US-0149010.
                                                                                                                                                                                            98US-0107466
                                                                                                                                                                                                    98US-0104585
                                                                                                                                                                                                                             99WO-US22955
                                                                                                                                                                                                                                                                                                              /note= "Cleavage site of leader sequence" 36..474
                                                                                                                                                                                                                                                                                              /note= "Human soluble CD39 protein"
                                                                                                                                                                                                                                                                                                                                           /label= Leader_peptide
/note= "Derived from human interleukin 2 (hIL2)"
                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.1%;
73.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 75; DB 21;
Pred. No. 0.00012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                              Gimpel SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21; Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY70888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                  13-OCT-1999;
                                   13-AUG-1999;
                                                                                                          27-APR-2000
                                                                                                                                  WO200023094-A2.
                                                                                                                                                                     Region
                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                            Region
                                                                                                                                                                                                        CLeavage-site
                                                         6-0CT-1998;
                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY70888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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Soluble CD39; ADP-induced platelet activation; platelet aggregation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; cursion; preeclampsia; embolism; cerebral ischaemia; thrombotic disorder; coronary artery thrombosis; cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis; peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT; PE; pulmonary embolism; transient ischaemic attack; thrombus formation; occlusion; reocclusion; stenosis; restenosis; antianginal; cardiant; cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
(IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          myocardial infarction, coronary artery disease or injury, embolism, atherosclerosis, peripheral vascular occlusion, preeclampsia, platelet-associated ischaemic disorders including lung, coronary and cerebral ischaemia, thrombotic disorders including coronary, peripheral and cerebral artery thrombosis, intracardiac and venous thrombosis, coagulopathy, deep venous thrombosis (DNT), pulmonary embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coronary ischaemia; vascular occlusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein encoded by CD39-L4-1 construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY70888 standard; Protein; 476 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADP-induced platelet activation and recruitment, including platelet aggregation. Soluble CD39 polypeptides are useful for inhibiting angiogenesis. It is useful for the treatment of unstable angina, stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       construct comprises of the leader peptide from human interleukin 2 (hIL2) and soluble CD39 (solCD39) protein region, having apyrase activity. Soluble CD39 is constructed by removing the N- and C-terminal transmembrane domains. It retains the capacity to metabolise AFP and ADP at relevant concentrations and the ability to block and reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              restenosis of blood vessels or stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 ETNNQETFGALDLGGASTQ 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KSDTQETYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          474 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                            98US-0104585
98US-0107466
                                                                                                                                                                                                                                                                        99WO-US23641
                                                                                                                            99US-0149010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 20..21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38..476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Soluble portion of CD39"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Derived from CD39-L4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.1%;
73.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.
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Pred. No. 0.00012;
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AAY70889
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                physiologically relevant concentrations as well as the ability to block and reverse ADP-induced platelet activation and recruitment including platelet aggregation. This is used in the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, platelet-associated ischaemic disorder including lung ischaemia, coronary ischaemia and cerebral ischaemia thrombotic disorder including coronary ischaemia and cerebral ischaemia, thrombotic disorder including coronary ischaemia artery thrombosis, venous thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis, thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibiting platelet activation and recruitment, useful for treating a mammal suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, comprises administering soluble CD39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a fusion construct of human soluble CD39 encoded by CD39-L4-1 construct. CD39-L4 is a secreted apyrase belonging to the CD39 family. The fusion construct is used for the expression and activity of soluble CD39 in CH0 (chinese hamster ovary) cells. Soluble CD39 retains the capacity of wildtype CD39 to metabolise ATP and ADP at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Page 89-91; 118pp; English.
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                                                                                                                                                                                                                                  unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; lung ischaemia; thrombolytic; coronary ischaemia; cerebral ischaemia; coronary artery thrombosis; cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis; peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DTT; peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DTT; peripheral artery thrombosis; restenosis; antianginal; cardiant; occlusion; reocclusion; stenosis; restenosis; antianginal; cardiant; cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       restenosis of blood vessels or stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein encoded by CD39-L4 construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY70889 standard; Protein; 476 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Soluble CD39; ADP-induced platelet activation; platelet aggregation;
                                                                   Location/Qualifiers
Misc-difference 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 ETNNQETFGALDLGGASTQ 220
                     Region
                                        Cleavage-site
                                                                                                                                                     Synthetic
                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                   thrombotic disorder; vascular occlusion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                        /note= "Any amino acid preferably Cys or Ser" 20..21
    /note= "Derived from CD39-L4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.1%; Score 75; DB 21; 73.7%; Pred. No. 0.00012;
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Search completed: February 11, 2003, 18:37:42

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Job time : 83 secs

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                                                                                  Matches
                                                                                                                      Query Match
                                                                                                  Best Local Similarity
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06-NOV-1998;
13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                recruitment including platelet aggregation. This is used in the treatment of unstable angina, myocardial infarction, stroke, coronary artery of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, disease or injury, atherosclerosis, peripheral vascular occlusion, preeclamgia, embolism, platelet-associated ischaemic disorder including thrombosis, coronary ischaemia and cerebral ischaemia, at thrombosic disorder including coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT), thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PB), transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis of restenosis of blood vessels or stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                            belonging to the CD39 family. The fusion construct is used for the expression and activity of soluble CD39 in CH0 (chinese hamster ovary) eclis. Soluble CD39 retains the capacity of wildtype CD39 to metabolise ATP and ADP at physiologically relevant concentrations as well as the ATP and ADP at physiologically relevant concentrations as well as the ATP and ADP induced platelet activation and ability to block and reverse ADP-induced platelet activation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a fusion construct of human soluble CD39 encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 91-93; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coronary artery disease or injury, comprises administering soluble CD39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibiting platelet activation and recruitment, useful for treating a mammal suffering from unstable angina, myocardial infarction, stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-339518/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maliszewski CR, Gayle RB, Marcus AJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                   Sequence
202 ETNNQETFGALDLGGASTQ 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD39-L4-2 and CD39-L4-3 constructs. CD39-L4 is a secreted
                                        1 KSDTQETYGALDLGGASTQ 19
                                                                                                                                                                       476 AA;
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0107466.
99US-0149010.
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                                                                                                         78.1%;
73.7%;
                                                                                       4; Mismatches
                                                                                                             Score 75; U
                                                                                                           Pred. No.
                                                                                                                                 DB 21;
                                                                                                             ,00012;
                                                                                                                                 Length 476;
                                                                                           Indels
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BioTech-Chem Library Search Results Feedback Form (Optional)

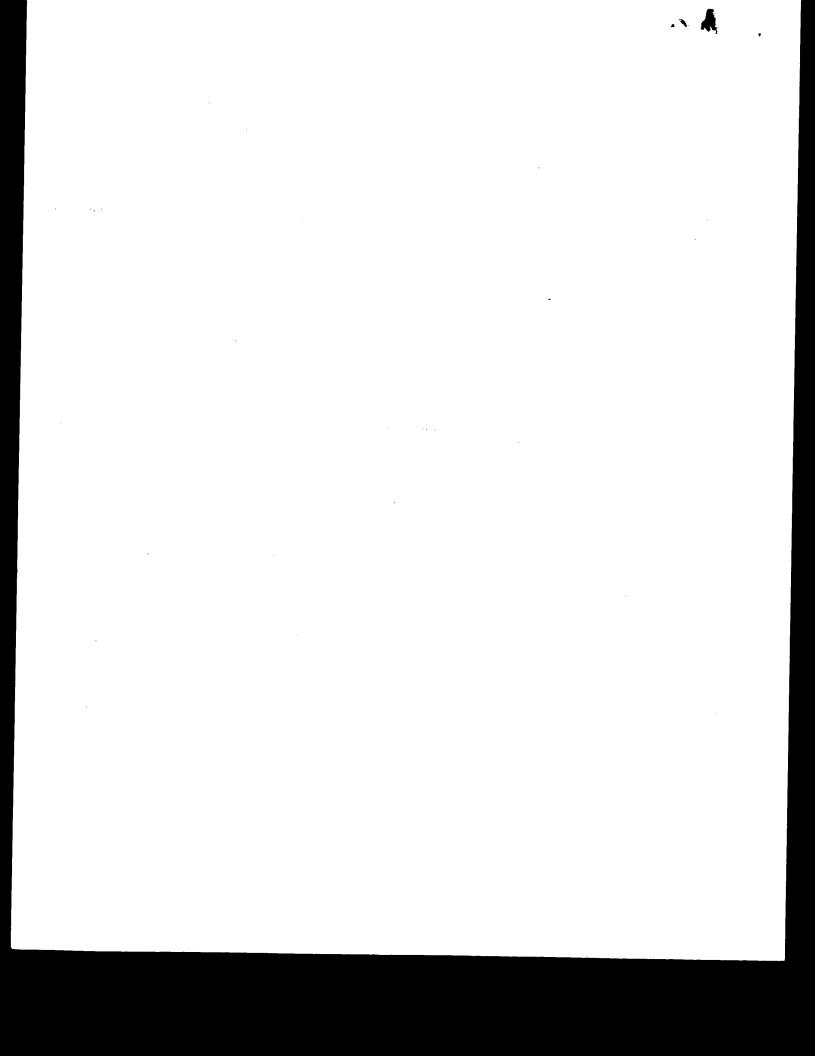
mary.hale@uspto.gov



The search results generated for your recent request are attached. If you have any questions or con (compliments or complaints) about the scope or the results of the search, please contact the BioTecsearcher who conducted the search or contact:

Mary Hale, Supervisor, 3: CM-1 Room 1E01

| Voluntary Results Feedback Form |
|--|
| > I am an examiner in Workgroup: (Example: 1610) |
| > Relevant prior art found, search results used as follows: |
| 102 rejection |
| 103 rejection |
| Cited as being of interest. |
| Helped examiner better understand the invention. |
| Helped examiner better understand the state of the art in their technology. |
| Types of relevant prior art found: |
| Foreign Patent(s) |
| Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.) |
| > Relevant prior art not found: |
| Results verified the lack of relevant prior art (helped determine patentability). |
| Search results were not useful in determining patentability or understanding the in |
| Other Comments: |
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| Drop off completed forms at the Circulation Desk CM-1, or send to Mary Hale, CM1-1E01 or |
| Drop off completed forms at the Circulation Desk Civility of Solid to Francy |



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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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  February 11, 2003, 18:36:22; Search time 30 Seconds (without alignments)
18.635 Million cell updates/sec
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Match Length DB
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
US-08-930-921-7
US-08-930-921-8
US-08-930-921-1
US-09-608-285A-25
US-09-608-285A-5
US-09-608-285A-7
US-09-608-285A-7
US-09-608-285A-7
US-09-608-285A-7
US-09-240-639-9
US-09-350-836B-3
US-09-350-836B-7
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                   NUMBER OF SEQ ID NOS:
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| RESULT 2 US-08-930-921-8 US-08-930-921-8 ; Sequence 8, Application US/08930921B ; Patent No. 6287837 ; GENERAL INFORMATION: APPLICANT: SEVIGUN, Jean APPLICANT: SEVIGUN, Jean APPLICANT: SEVIGUN, Jean APPLICANT: SEVIGUN, Jean APPLICANTION: THEREOF AND PROCESS OF PRODUCING TITLE OF INVENTION: THEREOF AND PROCESS TITLE OF INVENTION: THEREOF AND PR | Query Match 100.0%; Score 96; DB 4; Length Best Local Similarity 100.0%; Pred. No. 2.1e-10; Matches 19; Conservative 0; Mismatches 0; Inde Qy 1 KSDTQETYGALDLGGASTQ 19 Db 1 KSDTQETYGALDLGGASTQ 19 | US-08-930-921-7 | ALIGNMENTS | 28 39 40.6 473 4 US-09-240-639-12 39 39.6 69 1 US-08-905-223-410 30 39.6 69 1 US-08-46-692-95 31 38 39.6 69 2 US-08-488-351A-95 32 38 39.6 332 2 US-08-637-7638-6 33 39.6 332 3 US-09-170-354-6 34 38 39.6 382 1 US-09-170-354-6 35 38 39.6 649 4 US-09-305-270-3 36 39.6 679 5 PCT-US93-03027-3 37 38.5 346 4 US-09-343-0118-2 38 37 38.5 346 4 US-09-343-0118-2 38 37 38.5 366 4 US-09-955-270A-21 38 37 38.5 366 4 US-09-955-270A-21 39 37 38.5 366 4 US-09-955-97-25 40 37 38.5 467 4 US-09-129-112-19 42 37 38.5 467 4 US-09-129-112-19 43 36.5 38.0 1548 4 US-09-376-330-15 44 36 37.5 123 2 US-08-665-202-30 |
|--|---|---|------------|--|
| OF PURIFICATION THEREOF BY RECOMBINANT | ngth 20; Indels 0; Gaps 0; | | | Sequence 12, Appl Sequence 95, Appl Sequence 95, Appl Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 14, Appl Sequence 3, Appli Sequence 2, Appli Sequence 21, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 51, Appl Sequence 30, Appl Sequence 31, Appl Sequence 31, Appl Sequence 30, Appl Sequence 31, |

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CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US/09/608,285A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                           ; Sequence 25, Application US/09608285A; Patent No. 6335013; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-608-285A-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                        APPLICANT: FORD, John
APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 1
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                                                                                                                                                                                                                                      FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BEAUDOIN, Adrien R.
APPLICANT: SEVIGNY, Jean
TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
TITLE OF INVENTION: TECHNOLOGY
FILE REFERENCE: ATP-DIPHOSPHOHYDROLASES-BEAUDOIN
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Best Local 9
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NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
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CURRENT FILING DATE: 1998-01-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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73.78;
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 Mismatches

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Pred. No. 4.2e-05;
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TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28111,75908
FILE REFERENCE: 28111,75908
CURRENT APPLICATION NUMBER: US/09/370,265
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: PCT/US99/16180
EARLIER APPLICATION NUMBER: 09/250,836
EARLIER APPLICATION NUMBER: 09/250,836
EARLIER APPLICATION NUMBER: 09/273,447
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-03-19
EARLIER FILING DATE: 1999-03-19
EARLIER FILING DATE: 1999-03-19
EARLIER APPLICATION NUMBER: 09/274,444
EARLIER APPLICATION NUMBER: 09/22,449
EARLIER APPLICATION NUMBER: 09/12,449
EARLIER APPLICATION NUMBER: 09/118,205
EARLIER APPLICATION NUMBER: 09/118,205
EARLIER APPLICATION NUMBER: 09/118,205
EARLIER APPLICATION NUMBER: 09/118,205
EARLIER FILING DATE: 1998-07-16
UNMBER OF SEQ ID NOS: 37
; Sequence 3, Application US/09608285A
                             US-09-608-285A-3
                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens US-09-370-265-25
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                                                                                                                                                                                                                               Matches
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PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/35
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/27
PRIOR FILING DATE: 1999-03-19
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PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 1999.02-04
PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 1998-07-24
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                                                                                                                                                                                                                                             Match 66.7%; Score 64; DB 4; Local Similarity 86.7%; Pred. No. 0.0026;
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PRIOR APPLICATION NUMBER: 09/583,231
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR FILING DATE: 2000-04-25
PRIOR REPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370,265
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US-09-608-285A-5
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PRIOR APPLICATION NUMBER: 09/27
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/24
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/12
PRIOR FILING DATE: 1998-07-24
PRIOR FILING DATE: 1998-07-24
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          PRIOR APPLICATION NUMBER: 09/55/
PRIOR APPLICATION NUMBER: 09/48/
PRIOR APPLICATION NUMBER: 09/48/
PRIOR FILING DATE: 2000-01-11/
PRIOR APPLICATION NUMBER: 09/37/
PRIOR FILING DATE: 1999-08-09/
PRIOR APPLICATION NUMBER: PCT/US
PRIOR APPLICATION NUMBER: 09/35/
PRIOR FILING DATE: 1999-07-16/
PRIOR FILING DATE: 1999-07-09/
PRIOR FILING DATE: 1999-07-09/
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GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: 09/273,447
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PatentIn Ver. 2.0
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Yeung, George
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Mulero, Julio
Yeung, George
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1999-07-09
ИОМЕРТ
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86.7%;
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US-09-608-285A-5
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US-09-608-285A-7
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PRIOR APPLICATION NUMBER: 09/24
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/11
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/11
PRIOR APPLICATION NUMBER: 09/11
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APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
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CURRENT APPLICATION NUMBER: US/09/608,285A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION
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ORGANISM: Homo sapiens
                                                                                            Query Match
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PRIOR APPLICATION NUMBER: 09/
PRIOR PILING DATE: 1990-02-04
PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 1998-07-24
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PRIOR FILING DATE: 2000-
PRIOR APPLICATION NUMBER:
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                                                               Matches
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PRIOR FILING DATE: 1999-07-09/
PRIOR APPLICATION NUMBER: 09/
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                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                               TYPE: PRT
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192 QETYGTLDLGGASTQ 206
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                                                                                 Local
                                 5 QETYGALDLGGASTQ 19
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                                                                                 Similarity
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86.7%;
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                                                                                    Score 64; DB 4;
Pred. No. 0.0028;
                                                                      Mismatches
                                                                                                        DB 4; Length 428;
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GENERAL INFORMATION:
APPLICANT: FORD, Julio
APPLICANT: MIGHOR, Julio
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
TITLE REFERENCE: 28110/35761
FULL REFERENCE: 28110/35761
CURRENT APPLICATION NUMBER: US/09/350,836B
CURRENT APPLICATION NUMBER: US/09/350,836B
CURRENT PILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR FILING DATE: 1999-03-19
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Patent No. 6387645
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APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna-Maria
TITLE OF INVENTION: METHODS AND C
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Patent No. 6350447
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CURRENT FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 29
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APPLICANT: Frischauf, Anna-Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
FILE REFERENCE: 9598-066
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TYPE: PRT
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Similarity 86.7%; Pred. No. 0.0028;
0: Mismatches 2; Indels
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PRIOR PILING DATE: 1998-07-16
PRIOR PELICATION NUMBER: 09/12
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/24
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 APPLICANT: FORD, John
APPLICANT: Mulero, Julio
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
TILE REFERENCE: 28110/35761
CURRENT APPLICATION NUMBER: US/09/350,836B
CURRENT FILLING DATE: 1999-07-09
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LENGTH: 428
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SEQ ID NO 3
LENGTH: 428
PRIOR APPLICATION NUMBER: 09/273,447
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SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Mulero, Julio
TITLE OF INVENTION: METHODS AND M
TITLE OF INVENTION: POLYPEPTIDES
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ORGANISM: Homo sapiens
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SOFTWARE: PatentIn Ver. 2.0
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PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 1999-02-04
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ORGANISM: Homo sapiens
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86.7%;
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Pred. No. 0.0028; ....
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Sequence 5, Application US/09370265
Patent No. 6447771
GENERAL INFORMATION:
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US-09-370-265-3
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CURRENT APPLICATION NUMBER: US/09/370,265
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: PCT/US99/16180
EARLIER FILING DATE: 1999-07-16
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-07-09
EARLIER APPLICATION NUMBER: 09/273,447
EARLIER APPLICATION NUMBER: 09/273,447
EARLIER APPLICATION NUMBER: 09/273,444
EARLIER APPLICATION NUMBER: 09/273,444
EARLIER FILING DATE: 1999-03-19
EARLIER APPLICATION NUMBER: 09/214,444
EARLIER FILING DATE: 1999-07-04
EARLIER FILING DATE: 1998-07-04
EARLIER FILING DATE: 1998-07-04
EARLIER APPLICATION NUMBER: 09/12,449
EARLIER APPLICATION NUMBER: 09/12,449
EARLIER APPLICATION NUMBER: 09/12,449
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APPLICANT: FORT, John
APPLICANT: Mulero, Julio
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
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Patent No. 6447771
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PRIOR APPLICATION NUMBER: 09/1
PRIOR FILING DATE: 1998-07-16
PRIOR APPLICATION NUMBER: 09/1
PRIOR FILING DATE: 1998-07-24
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APPLICANT: Ford, John
APPLICANT: Mulero, Julio
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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TYPE: PRT
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                                                                                                                                                                                                                                                                                   5 QETYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                      Match 66.7%; Score 64; DB 4; Length 428; Local Similarity 86.7%; Pred. No. 0.0028; Local Similarity 86.7%; Pred. No. 0.0028; Indels les 13; Conservative 0; Mismatches 2; Indels
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EARLIER APPLICATION NUMBER: 09/350,836
EARLIER FILING DATE: 1999-07-09
EARLIER APPLICATION NUMBER: 09/273,447
EARLIER FILING DATE: 1999-03-19
EARLIER FILING DATE: 1999-03-14
EARLIER FILING DATE: 1999-02-04
EARLIER APPLICATION NUMBER: 09/212,449
EARLIER APPLICATION NUMBER: 09/122,449
EARLIER FILING DATE: 1998-07-24
EARLIER APPLICATION NUMBER: 09/118,205
EARLIER APPLICATION NUMBER: 09/118,205
EARLIER TILING DATE: 1998-07-16
NUMBER: 09/118,205
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                                                                                                                                               Query Match
                                                                                                 Matches
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FILE REFERENCE: 28111/35908
CURRENT APPLICATION NUMBER: US/09/370,265
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: PCT/US99/16180
EARLIER FILING DATE: 1999-07-16
                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                           LENGTH: 428
192 QETYGTLDLGGASTQ 206
                                                                                                                    Local Similarity
                                                5 QETYGALDLGGASTQ 19
                                                                                                   13;
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd.
KSDTQETYGALDLGGASTQ 19
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10 US-09-835-147-27
11 US-09-835-147-27
11 US-09-835-147-28
12 US-09-835-147-3
13 US-09-835-147-3
14 US-09-835-147-8
10 US-09-835-147-8
10 US-09-835-147-26
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40.452 Million cell updates/sec
 Sequence 2, Appli
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Sequence 7, Appli
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| RESULT 2 US-09-835 ; Sequeno ; Sequeno ; Patent ; GENERAL APPLIC ; APPLIC ; APPLIC ; APPLIC ; APPLIC ; APPLIC ; TIPL F ; FILE F ; FILE F ; CURREN ; CURREN ; CURREN | Query Ma Best Loc Matches Qy 1 Db 165 | RESULT 1 US-09-374-586 US-09-374-586 US-09-374-586 US-09-374-586 US-09-374-586 US-09-374-586 US-09-374-586 | | 20 20 21 22 22 23 24 24 24 24 24 24 24 24 24 24 24 24 24 |
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| ESULT 2 Sequence 6, Application US/0 Patent No. US20020002277A1 GENERAL INFORMATION: APPLICANT: Maliszewski, Cha APPLICANT: Bayle III, Rich APPLICANT: Edyle III, Rich APPLICANT: Erice, Virginia APPLICANT: Gimpel, Steven TITLE REFERENCE: 2879-US CURRENT APPLICATION NUMBER: CURRENT APPLICATION NUMBER: PRIOR APPLICATION NUMBER: | arity onser GALDL GALDL | pplicat. 2003013; anariou. insky, l enviou. enviou. ce: 057 ICATION OG DATE OG ID NO tentin | | 55555555555555555555555555555555555555 |
| Joon US/0983 2277A1 2277A1 II, Richard III, Richard Virginia L Virginia L Steven D. Steven D. Steven D. Steven D. Steven D. UMBER: US | 78 73 vativ GGAST | n US 58A1 vid D39/ SCHE 5916 UMBE 1999 1999 | | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 |
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| 35147 3 | ; Score 75; DB 10; Length; Pred. No. 4.2e-05; indel 4; Mismatches 1; Indel 9 | 74586 -ADPASE AS A TREATMEN DISORDERS S/09/374,586 | ALIGNMENTS | US-10-091-085-7 US-10-092-063-39 US-09-203-39-104-4 US-09-925-299-876 US-10-174-590-496 US-10-175-737-496 US-10-175-738-496 US-10-175-738-496 US-10-176-482-496 US-10-176-757-496 US-10-176-757-496 US-10-176-757-496 US-10-174-577-496 US-10-174-579-496 US-10-174-579-496 US-10-174-582-496 US-10-174-582-496 US-10-174-582-496 US-10-174-582-496 US-10-175-749-496 US-10-175-749-496 US-10-175-749-496 US-10-175-749-496 US-10-175-749-496 US-10-175-743-496 US-10-175-743-496 US-10-175-743-496 US-10-175-743-496 US-10-175-743-496 US-10-176-488-496 |
| and Recruitment | n 439; Hels 0; Gaps | | | Sequence 7, App Sequence 39, App Sequence 416, A Sequence 496, A |
| | 0; | | | App |

PRIOR APPLICATION NUMBER: US 60/104,585

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; Sequence 27, Application US/09835147; Patent No. US20020002277A1; GENERAL INFORMATION:
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PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 31
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PRIOR FILING DATE: 1999-08-13
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PRIOR FILING DATE: 1998-11-06
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CURRENT FILING DATE: 2001-04-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE REFERENCE: 2879-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gayle III, Richard B. APPLICANT: Price, Virginia L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Maliszewski, Charles R.
                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Fusion OTHER INFORMATION: construct of human CD39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 31
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PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
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Local Similarity 73.7%;
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73.7%;
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Pred. No. 4.5e-05;
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PRIOR FILING DATE: 1998-11-06
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PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR ETLING DATE: 1999-08-13
PRIOR ETLING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 31
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                        SEQ ID NO 29
LENGTH: 473
                                                    Matches
                                                                                               Query Match
                                                                         Best Local Similarity
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APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Gripel, Steven D.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
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                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Fusion OTHER INFORMATION: construct of human CD39
                                                                                                                                                                                                                           FEATURE:
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PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1999-08-13
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CURRENT APPLICATION NUMBER: US/09/835,147
CURRENT FILING DATE: 2001-04-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 31
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TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 ETNNOETFGALDLGGASTO 208
1 KSDTQETYGALDLGGASTQ 19
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                                            14; Conservative
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                                                            78.1%; Score 75; DB 10; Length 473; 73.7%; Pred. No. 4.6e-05;
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                                            4; Mismatches
                                       Indels
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                                    Gaps
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                                                                                                                       PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 31
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SEQ ID NO 28
LENGTH: 474
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APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Ginpel, Steven D.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
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PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1999-08-13
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CURRENT FILING DATE: 2001-04-13
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                                                                                    SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
FILE REFERENCE: 2879-US
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Maliszewski, Charles R. APPLICANT: Gayle III, Richard B. APPLICANT: Price, Virginia L. APPLICANT: Gimpel, Steven D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence FEATURE:
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                                                                                                     SOFTWARE: PatentIn Ver. 2.0
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                                          TYPE: PRT
FEATURE:
                                                              LENGTH:
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Local Similarity 73.78;
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; OTHER INFORMATION: Description of Artificial Sequence: Fusion ; OTHER INFORMATION: construct of human CD39 US-09-835-147-3
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PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: PCT/US99/22955
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APPLICANT: Gimpel, Steven D.
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                                                                                                                         APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Ginpel, Steven D.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
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                     FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KSDTQETYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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Price, Virginia L.
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73.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
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; GENERAL INFORMATION: APPLICANT: Ford, John
                                                            Sequence 38, Application US/10092063; Patent No. US20020173005A1
                                                                                                     US-10-092-063-38
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                                                                                                                                  RESULT 11
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PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
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PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEC ID NOS: 31
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      APPLICANT:
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SEQ ID NO 26
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TITLE OF INVENTION: Inhibitors of platelet Activation and Recruitment FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147
CURRENT FILING DATE: 2001-04-13
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Maliszewski, Charles R. APPLICANT: Gayle III, Richard B. APPLICANT: Price, Virginia L.
                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                     14; Conservative
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Mulero, Julio
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                                                                                                                                                                                                                                                                                  78.1%; Score 75; DB 10; 73.7%; Pred. No. 4.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.1%; Score 75; DB 10; Length 478; 73.7%; Pred. No. 4.6e-05; Indels
                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                  DB 10; Length 487;
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                                                                                        Matches
                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                          SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09835147
Patent No. US20020002277A1
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1999-08-13
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                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
FILE REPERENCE: 2879-US
                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/104,585 PRIOR FILING DATE: 1998-10-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/835,147
CURRENT FILING DATE: 2001-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR PILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350,836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-03-19
                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/122,449 PRIOR FILING DATE: 1998-07-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/244,444
PRIOR FILING DATE: 1999-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/370,265 PRIOR FILING DATE: 2002-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/092,063
CURRENT FILING DATE: 2002-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES FILE REFERENCE: 28110/35908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
202 ETNNQETFGALDLGGASTQ 220
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                                     1 KSDTQETYGALDLGGASTQ 19
                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KSDTQETYGALDLGGASTQ 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/118,205
FILING DATE: 1998-07-16
                                                                                     14;
                                                                                                                                                                                                                                   510
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                                                                                 Conservative
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                                                                                               78.1%; Score 75; DB 10; Length 510; 73.7%; Pred. No. 5e-05;
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                                                                            Mismatches
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; ORGANISM: HOMO-SAPIEN US-09-374-586-1
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US-10-092-063-25
: Sequence 25, Application US/10092063
: Patent No. US20020173005A1
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PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR EPLICATION NUMBER: 09/350,836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR APPLICATION NUMBER: 09/274,444
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-02-04
PRIOR FILING DATE: 1999-02-04
; Sequence 3, Application US/10092063
                        US-10-092-063-3
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APPLICANT: Pinsky, David J.
TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
TITLE OF INVENTION: ISCHEMIC DISORDERS
TILE REFERENCE: 0575/59167
CURRENT APPLICATION NUMBER: US/09/374,586
CURRENT FILING DATE: 1399-08-13
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1.2
                                                   RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 25
LENGTH: 405
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TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
ETILE REFERENCE: 28110/35908
                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                        Query Match
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PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/092,063
CURRENT FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: 09/370,265
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                                                                                                                         192 QETVGTLDLGGASTQ 206
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                                                                                                                                                                       5 QETYGALDLGGASTQ 19
                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                          66.7%; Score 64; DB 9; Length 405; B6.7%; Pred. No. 0.0027; ative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 510;
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; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 3
search completed: February 11, 2003, 18:47:24 Job time : 13 secs
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PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/244,444
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/122,449
PRIOR FILING DATE: 1998-07-24
PRIOR FILING DATE: 1998-07-16
PRIOR FILING DATE: 1998-07-16
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                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Mulero, Julio TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES FILE REFERENCE: 28110/35908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 2002-01-31
PRIOR PPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350,836
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/092,063
CURRENT FILING DATE: 2002-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ford, John APPLICANT: Mulero, Ju
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 428
                                                                                                       192 QETVGTLDLGGASTQ 206
                                                                                                                                                            5 QETYGALDLGGASTQ 19
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Post-processing: Minimum Match 0%
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Maximum DB seq length: 2000000000
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Perfect score:
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96
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/cgn2_6/ptodata/1/paa/USO83_COMB.pep:*
/cgn2_6/ptodata/1/paa/US60_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 6 | υ 🏊 | ων | - | Result No. |
|--------------------|--|---|-------------------|-----------------------------|
| 75 | 75 75 | 75 75 | 96 | Score |
| 78.1 | 78.1 78.1 | 78.1 | 100.0 | Query Match |
| 454 | 439 | 276 | 19 | Query Match Length DB ID |
| - | 17 | 19 | 21 | BB |
| 1 PCT-US99-22955-6 | US-09-374-586-2 | US-09-781-7968-8 US-09-558-630A-30 | US-09-781-796B-7 | Length DB ID |
| Sequence b, Appli | Sequence 2, Appli Sequence 2, Appli | Sequence 0, Appli Seguence 30, Appli | Sequence 7, Appli | Description |

Query Match

100.0%; Score 96; DB 21; Length 19;

| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | ω ω | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 1: | 10 | 9 (| 20 - | 7 |
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| 69 | 69 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 | 75 |
| 71.9 | 71.9 | 78.1 | 78.1 | 78.1 | 78.1 | 78.1 | 78.1 | 78.1 | 78.1 | 78.1 | 78.1 | 78.1 | 8 | 78.1 | 78.1 | æ | 78.1 | 8 | 8 | 78.1 | 8 | | 8 | 8 | 8 | в. | 8 | ω. | ω. | 8 | ω. | 78.1 | 8 | | 78.1 | 78.1 | | 78.1 |
| 120 | 120 | 510 | 510 | 510 | 510 | 510 | 510 | 510 | 510 | | | | | | | | 478 | | | | | | | | | | | | | | | 464 | | 63 | 63 | 63 | 4 | 4 |
| 22 | 22 | 22 | 22 | 21 | 17 | 1 | H | 1 | ۲ | 24 | 19 | 17 | 22 | 22 | _ | 22 | 22 | _ | 22 | 22 | 22 | 22 | 1 | سا | 22 | 22 | | 22 | 22 | ۳4 | 22 | | | 22 | 22 | هسو | 22 | 22 |
| US-09-834-366-1/02/ | 5-09-834-366-1702 | 09 835 147-2 | -09-807-660A- | -T87-60- | -09-374-586-L | US-08-701-460-4 | -08-701-460- | PCT-US99-22955-2 | PCT-US00-22060-1 | US-10-092-063-38 | US-09-557-800C-55 | 370-625A- | -09-835-147-2 | US-09-807-660A-26 | PCT-US99-22955-26 | 5-147-8 | 807-660A | PCT-US99-22955-8 | 5-147- | | US-09-807-660A-4 | US-09-807-660A-3 | PCT-US99-22955-4 | PCT-US99-22955-3 | US-09-835-147-28 | 7- | -US99-22955-2 | US-09-835-147-29 | US-09-807-660A-29 | 1 | -09-835-14 | -09-807-660A- | -US99-22 | -09-835-147-3 | US-09-807-660A-30 | T-US99-22955- | -09-835-1 | US-09-807-660A-6 |
| sequence 1/02// A | 0 17027 | 0 (1 | 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | ر ب د | - + | ء د | - ^ | ۰ د | , <u>-</u> | ຸດ | | 1 4 | e 26, | 26, | 26, A | ο, α | g, Appr | 8, Appli | о 4. | J, Appi | 4, Appi | 3, Appı | , <u>,</u> | ٠ س | , 2. 9 | 28, | 28, 7 | 29, | • | 29, 1 | Sequence 27, Appl | 27, | , | 30, | 30, | 30, | , | Sequence 6, Appli |

ALIGNMENTS

US-09-781-796B-7

RESULT 1

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; APPLICANT:
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US-09-781-796B-7
                                                                                                                                   PRIOR APPLICATION NUMBER: 08/
PRIOR FILING DATE: 1998-02-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                        ; SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ROBSON, Simon
TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
TITLE OF INVENTION: TECHNOLOGY
FILE REFERENCE: 920333.90019
                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER US/09/781,796B
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 08/419,204
PRIOR FILING DATE: 1995-04-10
PRIOR APPLICATION NUMBER: CA96/00223
PRIOR FILING DATE: 1996-04-10
PRIOR FILING DATE: 1996-04-10
                              ORGANISM: Porcine
                                                                            LENGTH: 19
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Best Local

Similarity

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B
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MINTZ, Liat et al.
TITLE OF INVENTION: ALTERNATIVE SPLICE VARIANTS
FILE REFERENCE: 2786-0150P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2000-04-26
NUMBER OF SEQ ID NOS: 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/558,630A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/781,796B CURRENT FILING DATE: 2001-02-12 PRIOR APPLICATION NUMBER: 08/419,204 PRIOR FILING DATE: 1995-04-10 PRIOR APPLICATION NUMBER: CA96/00223 PRIOR FILING DATE: 1996-04-10 PRIOR F
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TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
TITLE OF INVENTION: TECHNOLOGY
EILE REFERENCE: 920333.90019
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                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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202 ETNNQETFGALDLGGASTQ 220
                                                                                                                                                                                             Local
                                                                       1 KSDTQETYGALDLGGASTQ 19
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                                                                                                                                                                            h 78.1%; Score 75; DB 19; Similarity 73.7%; Pred. No. 0.00043;
                                                                                                                                                       Conservative
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                                                                                                                                                   4; Mismatches
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                                                                                                                                                                                                              DB 19; Length 276;
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PCT-US00-22060-2 RESULT 4

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                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
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                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application PC/TUS9922955 GENERAL INFORMATION:
                                                                                                                                                                                                                   APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Cimpel, Steven D.
APPLICANT: Immunex Corporation
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
NUMBER OF SEQ ID NOS: 31 SOFTWARE: Patentin Ver.
                                 EARLIER APPLICATION NUMBER: US 60/107,466 EARLIER FILING DATE: 1998-11-06 EARLIER APPLICATION NUMBER: US 60/149,010 EARLIER FILING DATE: 1999-08-13
                                                                                                                                                             CURRENT APPLICATION NUMBER: PCT/US99/22955
CURRENT FILING DATE: 1999-10-13
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SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application PC/TUS0022060 GENERAL INFORMATION:
                                                                                                                      EARLIER APPLICATION NUMBER: US 60/104,585 EARLIER FILING DATE: 1998-10-16
                                                                                                                                                                                                              FILE REFERENCE: 2879-WO
                                                                                                                                                                                                                                                                                                                              APPLICANT: Maliszewski, Charles R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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TITLE OF INVENTION: CD39/EC
TITLE OF INVENTION: ISCHEMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: PCT/US00/22060 CURRENT FILING DATE: 2000-08-11
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73.7%;
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Pred. No. 0.00076;
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PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
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CURRENT APPLICATION NUMBER: US/09/835,147
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1999-08-13
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                                                                                                                                                                                                                            Sequence 6, Application US/09835147
GENERAL IMPORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
APPLICANT: APPLICANT: TANNAMENAL TANNAMENAL
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APPLICANT: Immunex Corporation
APPLICANT: Cornell Research Foundation, Inc.

TITLE OF INVENTION: Methods of Inhibiting Platelet Activation and
TITLE OF INVENTION: Recruitment
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CURRENT FILING DATE: 2001-04-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                      TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE REFERENCE: 2879-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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TYPE: PRT
ORGANISM: Artificial Sequence
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Local Similarity 73.7%;
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Local Similarity 73.7%;
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Pred. No. 0.00079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 75; DB 22; pred. No. 0.00079;
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; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 6
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CURRENT FILING DATE: 1999-10-13
EARLIER APPLICATION NUMBER: US 60/104,585
EARLIER FILING DATE: 1998-10-16
EARLIER APPLICATION NUMBER: US 60/107,466
EARLIER FILING DATE: 1998-11-06
EARLIER FILING DATE: 1998-11-06
EARLIER FILING DATE: 1998-13
NUMBER OF SEQ ID NOS: 31
NUMBER OF SEQ ID NOS: 31
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; Sequence 30, Application PC/TUS9922955
; GENERAL INFORMATION:
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APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
APPLICANT: Immunex Corporation
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
FILE REFERENCE: 2879-WO
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ORGANISM: Artificial Sequence
FILE REFERENCE: 23,495 PCT
                                                                                                                       APPLICANT: Maliszewski, Charles R. APPLICANT: Gayle III, Richard B. APPLICANT: Marcus, Aaron J.
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                                 TITLE OF INVENTION: Methods of Inhibiting Platelet Activation and TITLE OF INVENTION: Recruitment
                                                                                 APPLICANT: Immunex Corporation
APPLICANT: Cornell Research Foundation, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                   78.1%; Score 75; DB 1; 73.7%; Pred. No. 0.00081;
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PCT-US99-22955-27

Sequence 27, Application PC/TUS9922955
GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
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PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SECTION 30
FENCHUL ACT
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                                                                                                                                                                                                                                          Matches
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PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-66
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CURRENT APPLICATION NUMBER: US/09/835,147
CURRENT FILING DATE: 2001-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Maliszewski, Charles R. APPLICANT: Gayle III, Richard B.
                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Fusion OTHER INFORMATION: construct of human CD39
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                                                                                                                                              189 ETNNQETFGALDLGGASTQ 207
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                                                                                                                                                                                                                                                             Local
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Local Similarity 73.7%;
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                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                          78.1%; Score 75; DB 22; Length 463; 73.7%; Pred. No. 0.00081;
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US-09-807-660A-27
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CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1999-08-13
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; LENGTH: 464
; TYPE: PRT
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                                                                                             Matches
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                                                                                                                                    Query Match
                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27,
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Methods of Inhibiting Platelet Activation and TITLE OF INVENTION: Recruitment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Maliszewski, Charles R. APPLICANT: Gayle III, Richard B. APPLICANT: Marcus, Aaron J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 23,495 PCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: US 60/104,585
EARLIER FILING DATE: 1998-10-16
EARLIER APPLICATION NUMBER: US 60/107,466
EARLIER FILING DATE: 1998-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
APPLICANT: Inmunex Corporation
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
FILE REFERENCE: 2879-WO
                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Fusion OTHER INFORMATION: construct of human CD39
                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: US 60/149,010 EARLIER FILING DATE: 1999-08-13 NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: PCT/US99/22955 CURRENT FILING DATE: 1999-10-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                     FEATURE:
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Fusion OTHER INFORMATION: construct of human CD39
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190 ETNNQETFGALDLGGASTQ 208
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                                         1 KSDTQETYGALDLGGASTQ 19
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                                                                                     14; Conservative
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Cornell Research Foundation, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                       78.1%; Score 75; DB 22; Length 464; 73.7%; Pred. No. 0.00081;
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73.7%;
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                                                                                     Mismatches
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CURRENT FILING DATE: US/09/835,147
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR PELING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: OS 60/149,010
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: OS 60/149,010
PRIOR FILING DATE: 1999-10-13
UNUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 464
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PCT-US99-22955-29
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                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Fusion ; OTHER INFORMATION: construct of human CD39 PCT-US99-22955-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 78.1%; Score 75; DB 22; Length 464; Best Local Similarity 73.7%; Pred. No. 0.00081; Matches 14; Conservative 4; Mismatches 1; Indels
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APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
FILE REFERENCE: 2879-US
                                                                                                                                                                                                                                                                                EARLIER FILING DATE: 1998-11-06
EARLIER APPLICATION NUMBER: US 60/149,010
EARLIER FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 29
Query Match 78.1%; Score 75; DB 1; Length 473; Best Local Similarity 73.7%; Pred. No. 0.00083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Maliszewski, Charles R. APPLICANT: Gayle III, Richard B. APPLICANT: Price, Virginia L. APPLICANT: Gimpel, Steven D. APPLICANT: Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: PCT/US99/22955
CURRENT FILING DATE: 1999-10-13
EARLIER APPLICATION NUMBER: US 60/104,585
EARLIER FILING DATE: 1998-10-16
EARLIER APPLICATION NUMBER: US 60/107,466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE REFERENCE: 2879-WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Fusion OTHER INFORMATION: construct of human CD39
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                     LENGTH: 473
TYPE: PRT
                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                            FEATURE:
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Matches 14; Conservative 4; Mismatches 1; Indels 0; G

Qy 1 KSDTQETYGALDLGGASTQ 19
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Db 199 ETNNQETEGALDLGGASTQ 217

Search completed: February 11, 2003, 18:46:40

Job time: 355 secs
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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 February 11, 2003, 18:38:07; Search time 19 Seconds
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1 KSDTQETYGALDLGGASTQ 19
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Match
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Copyright (c) 1993 - 2003 Compugen Ltd.
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 //cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
//cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*
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//cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*
//cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*
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   US-09-724-676-59001
US-09-724-676-59000
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US-09-724-676-59000
US-09-835-147A-30
US-09-835-147A-29
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US-09-835-147A-8
US-09-835-147A-2
US-09-835-147A-2
US-09-835-147A-2
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US-09-835-147A-2
US-09-724-676-58998
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83.231 Million cell updates/sec
                                             sequence 30, Appl
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Sequence 6, Appli
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Sequence 58999, A
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           1 KSDTQETYGALDLGGASTQ 19
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| Query Match Best Local Matches 1 | IESULT 2 Sequence 590 GENERAL INFO APPLICANT: TITLE OF IN FILE REFERE CURRENT APP CURRENT APP CURRENT FIL NUMBER OF II NUMBER OF II NUMBER OF II NUMBER OF II NO 55 SOFTWARE: LENGTH: 27 TYPE PRT ORGANISM ORGANIS | Query Match Best Local S Matches 14 Matches 15 Matches 16 Matches 17 Matches 17 Matches 17 Matches 18 Match | SULT 1 5-09-724-676-59001 5-09-724-676-59001 5-09-724-676-59001 GENERAL INFORNATION: IND APPLICANT: COMPUSE IND TITLE OF INVENTION: Vari- FILE REFERENCE: 129181.4 CURRENT APPLICATION NUMBER OF SEQ ID NOS: 97 NUMBER OF SEQ ID NOS: 97 SOFTWARE: PATENTIN VETSI SEQ ID NO 59001 LENGTH: 276 TYPE: PRT ORGANISM: Homo Sapiens S-09-724-676-59001 | | 27 28 28 29 29 30 31 31 47 32 47 34 47 35 47 36 47 37 47 37 47 47 38 47 47 47 48 49 49 49 49 49 49 49 49 49 49 49 49 49 |
|---|--|--|---|------------|--|
| h Similarity 14; Conser | 59001 01, Appl: RMATION: ROMATION: NOCE: 129: NICE: 1 | imi QET | 576-59001 59001, Applicat IMFORMATION: DWT: Compugen LTD WT: Compugen LTD WT: Compugen LTD WT: COMPUGEN LY FERENCE: 129181. APPLICATION NUM FILING DATE: 20 F SEQ ID NOS: 9 E: Patentin vers 0 59001 276 FRT SM: Homo sapiens 676-59001 | | 54.2 54.2 54.2 49.0 49.0 49.0 49.0 49.0 49.0 49.0 47.9 47.9 |
| 78.1 y 73.7 rvative | tior D riam riam 2000 972: | 8.1 3.7 70 70 70 | LTD LTD Variants of 181.4 Compus NUMBER: US. : 2000-11-: S: 97222 version 3.2 | | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 |
| %; Score 75; DB 5; Len %; Pred. No. 0.00013; 4; Mismatches 1; | us/09724676A nts of alternative splicing Compugen R: US/09/724,676A 0-11-28 0-3.2 | ; Score 75; DB 5; Len; pred. No. 0.00013; ; 4; Mismatches 1; 9 | ion US/09724676 iants of alternative splicing Compugen 18709/724,676 1000-11-28 1100 3.2 | ALIGNMENTS | US-10-174-575A-496 US-10-187-749-496 US-10-187-749-496 US-10-199-672-496 US-09-724-676A-76017 US-09-724-676A-76019 US-09-724-676A-76019 US-09-724-676A-76016 US-09-724-676A-76018 US-09-724-676A-76018 US-09-724-676A-76018 US-09-724-676A-76018 US-09-724-676A-76018 US-09-724-676A-76018 US-09-724-676A-59094 US-09-724-676A-59094 US-09-724-676-59085 US-09-724-676-59085 US-09-724-676-59088 US-09-724-676-59088 |
| 276; els 0 | | gth 276; Indels 0; | | | Sequence seq |
| ; Gaps | | Gaps | | | 496, App 496, App 496, App 496, App 76017, A 76019, A 76019, A 76018, A 76018, A 76018, A 76018, A 76018, A 76018, A 750018, A 750018, A 59085, A 59085, A |
| 0; | | 0; | | | |

202 ETNNQETFGALDLGGASTQ 220

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GENERAL INFORMATION:

APPLICANT: Pinsky, David J.

TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND TITLE OF INVENTION: ISCHEMIC DISORDERS
FILE REFERENCE: 0575/59167
                                                                                                                                                                                                                                                                                                        US-10-049-420-2
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                                                               SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 2
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                                                                                                                                                                                                                                                                                Sequence 2, Application US/10049420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181 4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 59000
                                                                                        CURRENT APPLICATION NUMBER: US/10/049,420 CURRENT FILING DATE: 2002-02-06 PRIOR APPLICATION UNMBER: US/09/374,586 NUMBER OF SEQ ID NOS: 2
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alterna
ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 59000
LENGTH: 283
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                                             ENGTH: 439
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                                                                                                                                                                                                                                                                                                                                                                            209 ETNNQETFGALDLGGASTQ 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 78.1%; Score 75; DB 5; Length 283; Local Similarity 73.7%; Pred. No. 0.00013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.1%; Score 75; DB 5; 73.7%; Pred. No. 0.00013;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5; Length 283;
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CURRENT APPLICATION UNBER: US/09/835,147A
CUGRENT FILING DATE: 2001-04-13
PRIOR APPLICATION UNBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR PLICATION UNBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR PLICATION UNBER: US 60/149,010
PRIOR APPLICATION UNBER: DET/US99/22955
PRIOR APPLICATION UNBER: DET/US99/22955
PRIOR FILING DATE: 1999-10-13
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Maliszewski, Charles R. APPLICANT: Gayle III, Richard B. APPLICANT: Price, Virginia L. APPLICANT: Gimpel, Steven D.
                                                                                                                                                                                                                                                                                                                      APPLICANT: Gimpel, Steven D.

TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT FILE REFERENCE: 2879-US
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PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 37
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PRIOR APPLICATION NUMBER: US 60/104.585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107.466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149.010
PRIOR FILING DATE: 1998-08-13
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TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 ETNNQETFGALDLGGASTQ 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.1%; Score 75; DB 5; 73.7%; Pred. No. 0.00022;
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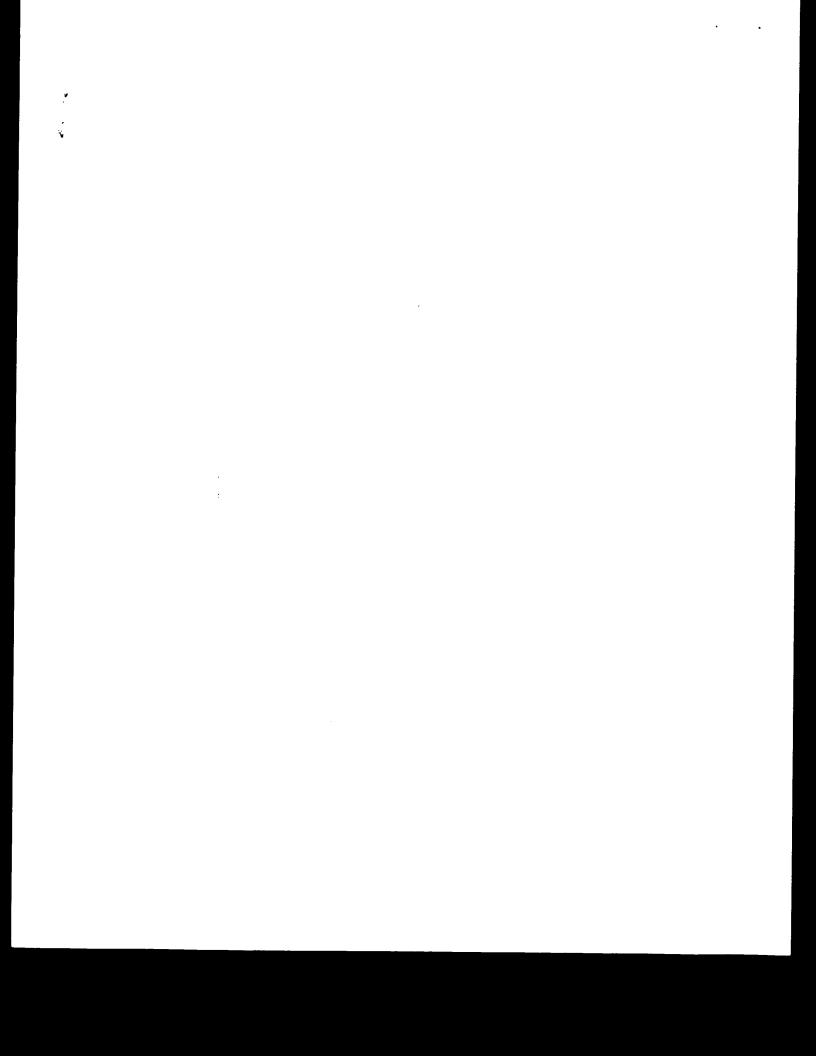
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, OTHER INFORMATION: Fusion construct of human CD39 08\text{-}09\text{-}835\text{-}147\text{A}\text{-}30
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CURRENT APPLICATION NUMBER: US/09/835,147A
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-13
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GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Gripei, Virginia L.
APPLICANT: Gimpei, Steven D.
TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
FILE REFERENCE: 2879-US
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APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Ginpel, Steven D.
TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
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PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1998-08-13
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CURRENT APPLICATION NUMBER: US/09/835,147A
CURRENT FILING DATE: 2001-44-13
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TYPE: PRT
ORGANISM: Artificial Sequence
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NUMBER OF SEQ ID NOS: 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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TYPE: PRT
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US-09-835-147A-29
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LENGTH: 474
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TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147A
CURRENT FILING DATE: 2001-04-13
CURRENT FILING DATE: 2001-04-13
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PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1998-08-13
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APPLICANT:
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PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 37
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                                                          APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gidmel, Steven D.
TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
FILE REFERENCE: 2879-US
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PRIOR APPLICATION NUMBER: US 60/104,585
                    CURRENT APPLICATION NUMBER: US/09/835,147A CURRENT FILING DATE: 2001-04-13
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                                                                                                                                                                                                                                                                                                             200 ETNNQETFGALDLGGASTQ 218
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Price, Virginia L.
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.1%;
73.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                  78.1%; Score 75; DB 5; Length 474; 73.7%; Pred. No. 0.00023;
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Pred. No. 0.00023
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; Sequence 8, Applicat;
; GENERAL INFORMATION:
                                       US-09-835-147A-8
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                                                                                                                                                                                                                                                                                     US-09-835-147A-4
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US-09-835-147A-4
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                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.1 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09835147A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Malissewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: price, Virginia L.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
FILE REFERENCE: 2879-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 37
SOTWARE: Patentin version 3.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/835,147A CURRENT FILING DATE: 2001-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Any amino acid, preferably Cys or Ser
                                                                                                                                                                                                                                                                                                                   NAME/KEY: MISC_FEATURE LOCATION: (39)...(39)
                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Fusion construct of human CD39
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                   202 ETNNQETFGALDLGGASTQ 220
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                                                                                                                                                                                                                            Local
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Local Similarity 73.7%;
                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 476
                                                                                                                                                                                                             h 78.1%; Score 75; DB 5;
Similarity 73.7%; Pred. No. 0.00023;
             Application US/09835147A
                                                                                                                                                                                               Conservative
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Pred. No. 0.00023;
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В
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PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1999-10-13
                                                                                                                                                                       , OTHER INFORMATION: Fusion construct of human CD39 US-09-835-147A-26
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                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.1 SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.1 SEQ ID NO 8
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PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1998-13
PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 37
                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Maliszewski, Charles R. APPLICANT: Gayle III, Richard B. APPLICANT: Price, Virginia L. APPLICANT: Gimpel, Steven D.
                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 37
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APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT FILE REFERENCE: 2879-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                    FEATURE:
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TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Maliszewski, Charles R. APPLICANT: Gayle III, Richard B. APPLICANT: Price, Virginia L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Fusion construct of human CD39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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213 ETNNQETFGALDLGGASTQ 231
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                                          1 KSDTQETYGALDLGGASTQ 19
                                                                                                       Match 78.1%;
Local Similarity 73.7%;
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                                                                                  14; Conservative
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                                                                                  4; Mismatches
                                                                                                Score 75; DB 5;
Pred. No. 0.00023;
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                                                                         0;
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WESULT 15
US-09-835-147A-2
ISEQUENCE 2, Application US/09835147A
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Gayle III, Richard B.
APPLICANT: Gimpel, Steven D.
TITLE DO INVENTION: INIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
CURRENT APPLICATION NUMBER: US/09/835,147A
CURRENT FILING DATE: 2001-04-13
CURRENT FILING DATE: 2001-04-13
CURRENT FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1998-10-13
INUMBER OF SED ID NOS: 37
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Title:
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                      pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                          46.5
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96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283224 seqs, 96134422 residues
                                                                                                                                                                                                                                                                                                                                                               Match Length DB ID
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                                                                                                                                                                                                                                                                                                                                                                           Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR_73:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
pir1:*
pir2:*
pir3:*
S50463
T39109
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S48859
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T40856
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114.160 Million cell updates/sec
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apyrase (EC 3.6.1.
propionyl coenzyme
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RESULT 3

| Qy 6 ETYGALDLGGASTQ 19 : Db 28 DLYGALDLGGASTQ 41 | Query Match 64.6%; Score 62; DB 2; Length Best Local Similarity 85.7%; Pred. No. 0.001; Matches 12; Conservative 1; Mismatches 1; Individual Conservative 1; Mismatches 1; Individual Conservative 1; Onservative 1; Mismatches 1; Individual Conservative 1; Individual Conservativ | RESULT 2 \$63501 sqyrase (EC 3.6.1.5) - human (fragments) N;Alternate names: ATP diphosphohydrolase C;Species: Homo sapiens (man) C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_ch C;Accession: \$63501 R;Christoforidis, S.; Papamarcaki, T.; Galaris, D.; Kellner Eur. J. Biochem. 234, 66-74, 1995 A;Title: Purification and properties of human placental ATP A;Reference number: \$63501; MUID:96096723; PMID:8529670 A;Accession: \$63501 A;Accession: \$63501 A;Residues: 1-3;4-8;9-13;14-20;21-30;31-44 <chr> C;Keywords: hydrolase</chr> | Qy 1 KSDTQETYGALDLGGASTQ 19 ::: : | Query Match 78.1%; Score 75; DB 2; Length Best Local Similarity 73.7%; Pred. No. 9e-05; Matches 14; Conservative 4; Mismatches 1; Independent of the conservative 4; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1 | ul-1996 # enborn, m antigen. pMID:793C | ALIGNMENTS | 30 40 41.7 425 2 H70456 31 40 41.7 485 2 T34147 32 40 41.7 522 2 B71978 33 40 41.7 590 2 A40437 34 40 41.7 808 2 E64914 36 40 41.7 808 2 E64914 37 39.5 41.1 463 1 I40661 37 39.5 41.1 463 1 I40661 38 39 40.6 227 2 S77870 39 40.6 294 2 B86703 40 39 40.6 294 2 G95077 41 39 40.6 311 2 D97945 42 39 40.6 315 2 F70203 43 39 40.6 505 1 S77034 44 39 40.6 518 2 A40732 45 39 40.6 518 2 A87518 |
|--|--|--|-------------------------------------|--|---|------------|--|
| | gth 44; Indels 0; Gaps 0; | _change 13-Mar-1997 .ner, R.; Tsolas, O. ATP diphosphohydrolase. | | gth 510; Indels 0; Gaps 0; | | | nodulation competi hypothetical prote hypothetical prote glutamic acid-rich dimethylsulfoxide hypothetical prote glucose transport mutt protein - Clo mutt protein - Clo trans type molecula trana isopentenyltr trana isopentenyltr xylose operon regu protein kinase pkn guanosine-diphosph hypothetical prote |

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A; Map position: 1
                                                                                                                                                 R:Barrell, B.G.; Rajandream, m.n., Cotober 1999
submitted to the EMBL Data Library, October 1999
A:Reference number: Z21828
A:Accession: 739109
                               A; Gene: SPDB:SPAC824.08
                                                                A; Experimental source: strain 972h-; cosmid c824
                                                                         A;Molecule type: DNA
A;Residues: 1-556 CBAR>
A;Cross-references: EMBL:AL121741; PIDN:CAB57338.1; GSPDB:GN00066; SPDB:SPAC824.08
                                                                                                                                               A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                        C;Accession: T39109
R;Barrell, B.G.; Rajandream, M.A.; Quail, M.; Seegar, K.; Harris, D.
                                                                                                                                                                                                                                                                 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                     probable guanosine-diphosphatase - fission yeast (Schizosaccharomyces pombe)
C; Species: Schizosaccharomyces pombe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: S50463
A;Molecule type: DNA
A;Residues: 1-630 <DIE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:U18778; NID:g603592; PID:g603597; GSPDB:GN00005; MIPS:YER005w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description: The sequence of S. cerevisiae cosmids 9537, 9581, 9495, 9867, and lambda A; Reference number: 850433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, December 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein YER005w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 28-May-1933 #sequence_revision 24-Feb-1995 #text_change 19-Apr-2002
C;Accession: S50463
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A;Residues: 1-1052 <BEV>
A;Cross-references: EMBL:AL021687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Dietrich, F.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Introns: 79/3; 1: A; Note: T18B16.150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein T18B16.150 - Arabidopsis thaliana (Forester are areas) C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: cultivar Columbia; BAC clone T18B16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: Z15359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Bevan, M.; Benes, V.; Rechmann, submitted to the Protein Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: T04439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                       179 TEGEMDMGGASTQ 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 TYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity es 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGD:YND1; MIPS:YER005w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.2%;
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76.9%;
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Sequence Database, April 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 52; DB 2
Pred. No. 0.99;
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Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 630;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                  A; Map position: 1
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A; Residues: 1-483 <STO>
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A; Residues: 1-557 <MIL>
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A; Accession: T16696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: T16696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
                                                                                                                                                          Query Match
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                               212 TDPLETTGIVELGGASAQ 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 QKTVGMIDMGGASAQ 226
                                                                                                                                      Local Similarity
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                                                                     2 SDTQETYGALDLGGASTQ 19
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                                                                                                                  Conservative
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                                                                                                                                 51.0%;
55.6%;
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62.5%;
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                                                                                                             3; Mismatches
                                                                                                                                 Score 49; DB Pred. No. 2.4;
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    Mismatches

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Chin, C.W.; Ching, M.K.; Coin, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A:Accession: D86276
                                                                                                                                                                                                                     A;Cross-references: GB:AE005172; NID:g5080801; PIDN:AAD39311.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F7A19.34 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Introns: 39/1; 67/1; 145/2; 192/1; 244/3; 317/3; 451/3; 488/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the EMBL Data Library, October 1995 ion: The sequence of C. elegans cosmid R07E4.
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                                                                     DB 2; Length 483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 557;
           5; Indels
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       0;
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Gaps
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   0;
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A:Title: Dictyostelium discoideum contains two profilin isoforms that differ in structur A; Reference number: A53255; MUID:92226170; PMID:1725525
A; Accession: B53255
A; Molecule type: mRNA
A; Residues: 1-124 (4NA2)
A; Cross-references: EMBL:X61580; NID:g7325; PIDN:CAA43780.1; PID:g7326
A; Cross-references: EMBL:X61580; NID:g7325; PIDN:CAA43780.1; PID:g7326
C; Keywords: actin binding; methylated amino acid
C; Keywords: actin binding; methylated amino acid
C; Keywords: actin binding; methylated amino acid
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C;Species: Dictyostelium discoideum
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 22-Jun-1999
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A; Residues: 1-572 <RAM>
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA .
                                                                    A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230 A;Accession: C70741
                                                                                                                                                                                 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C:Accession: C70741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:AL121783; PIDN:CAB57847.1; GSPDB:GN00068; SPDB:SPCC11E10.05c
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                                                                                                                                                                                                                                                R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein Rv1356c - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                Species: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 EKDT-STVGFLDMGGASVQ 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.4%; Score 46.5; DB 2; Length 572; 57.9%; Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
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Pred. No.
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R:Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R. Nucleic Acids Res. 23, 2105-2119, 1995
A:Title: Analysis of the Escherichia coll genome VI: DNA sequence of the region from A;Reference number: S56314; MUID:95334362; PMID:7610040
A:Accession: S56505
R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A, Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID: 21016719; PMID: 11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: B65241
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
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A;Cross-references: GB:Z75555; GB:AL123456; NID:g3261608; PIDN:CAA99989.1; PID:g14190
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                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F14L17.1 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Paceies: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001 C;Paccession: E86276
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A;Experimental source: strain K-12, substrain MG1655
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A; Residues: 1-377 <BLAT>
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N;Alternate names: hypothetical protein o377
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57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, M.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable nucleoside triphosphatase [imported] - Arabidopsis thaliana
(;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleoside triphosphatase precursor, chromatin-associated - garden pea C;Species: Pisum sativum (garden pea) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-Sep-1999 C;Accession: S65147; S48859 R;Hsieh, H.L.; Tong, C.G.; Thomas, C.; Roux, S.J. Plant Mol. Biol: 30, 135-147, 1996 A;Title: Light-modulated abundance of an mRNA encoding a calmodulin-regulated, chromatin A;Reference number: S65141; MUID:96197404; PMID:8616230 A;Accession: S65147
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                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-516 <STO>
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                                                                                                                                                                                                                                                         C; Genetics:
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A; Residues: 1-455 <HS2>
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A; Residues: 1-405 <STO>
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211 DPLKTTGIVELGGASAQ 227
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                                                                                                                            Local Similarity
                                                3 DTQETYGALDLGGASTQ 19
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Local Similarity 57.1%;
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Local Similarity 52.9%;
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                                                                                                                    Score 44;
Pred. No.
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Pred. No. 14;
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. A; Status: preliminary
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A;Experimental source: human B-type strain AG876JS; human B-type strain L4MR
A;Note: sequence extracted from NCBI backbone (NCBIN:79237, NCBIP:79254, NCBIN:79234,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Sequence variation of cytotoxic T cell epitopes in different isolates of Eps A;Reference number: A49034; MUID:92111623; PMID:1370413 A;Accession: G49553
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A;Residues: 1-925 <SAN>
A;Residues: 1-925 <SAN>
A;Cross-references: EMBL:M34440; NID:g330407; PIDN:AAA45893.1; PID:g330408
R;Apolloni, A; Moss, D.; Stumm, R.; Burrows, S.; Suhrbier, A.; Misko, I.; Schmidt, C
Eur. J. Immunol. 22, 183-189, 1992
Eur. J. Immunol. 22, 183-189, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nuclear antigen EBNA-3A - human herpesvirus 4
C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000
C;Accession: S27920; G49253; H49253; F49253
R;Sample, J.; Young, L.; Martin, B.; Chatman, T.; Kieff, E.; Rickinson, A.; Kieff, E. submitted to the EMBL Data Library, July 1990
                                                                                                                                                                                                                                                                                                                                                                              A;Introns: 112/3
C;Superfamily: human herpesvirus 4 nuclear antigen EBNA-3A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Cross-references: GB:S79235; NID:g242901; PIDN:AAB20990.1; PID:g242902
A:Experimental source: human B-type strain QIMR-JSM6
A:Note: sequence extracted from NCBI backbone (NCBIN:79235, NCBIP:79252)
A:Accession: H49253
Job time : 18 secs
                                Search completed: February 11, 2003, 18:40:02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 314-338 <AP2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
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A;Accession: S27920
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                                                                                                                                 829 RSDTSEPYEALDL 841
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                                                                                                                                                                                                                                                    9;
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    Mismatches

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Copyright (c) 1993 - 2003 Compugen Ltd.
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ENP3_HUMAN
ENP1_CHICK
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ENP1_BOVIN
ENP1_HUMAN
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ENP2_MOUSE
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ENP5_MESAU
YNFE_ECOLI
SNF3_YEAST
MIAA_LACLA
MIAA_STRPN
                                                                                           ENP6_HUMAN
RK3_GUITH
YD56_MYCTU
YJHC_ECOLI
NTPA_PEA
APY_SOLTU
ZN35_HUMAN
PRS4_DROME
YY4E_CAEEL
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ENP4_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
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Q21815 caenorhabdi
Q9er31 rattus norv
Q9dbt4 mus musculu
P26200 dictyosteli
                                                                                                                                                                                                                                                                                                                                                                                                                                          O93295 gallus gall
O99513 homo sapien
O55026 mus musculu
O35795 rattus norv
P79784 gallus gall
                                                                     Q11026 mycobacteri
p39353 escherichia
p52914 pisum sativ
p80595 solanum tub
p1568 homo sapian
p46601 drosophila
Q18411 caenorhabdi
p77374 escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9qyc8
Q9wuz9
Q75356
075355
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Q18956 bos taurus
                                                                                                                                                                                                                                    046894
Q11026
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P97687 rattus norv
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5 gallus gall
3 homo sapien
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         streptococc
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                                                      saccharomyc
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| DCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC | RESU ID AC DT DT DT DE DE OC | |
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| | RESULT 1 ENPL_PIG ID ENP AC Q9M AC 16- DT 16- DT 16- ENPL ENP CO ENT CO SUSTINIA | 35 35 37 37 38 39 40 41 42 42 43 |
| [1] SEQUENCE FROM N.A. TISSUE-AORTIC endothelium; TISSUE-AORTIC endothelium; MEDLINE-20325090; PubMed=10866813; MEDLINE-20325090; PubMed=10866813; MEDLINE-20325090; PubMed=10866813; MEDLINE-30325090; PubMed=10866813; Lemmens R., Vanduffel L., Kittel A., Be Sevigny J.; TISSUE-Fancreas; PubMed=8955160; MEDLINE-97115858; PubMed=8955160; MEDLINE-97115858; PubMed=8955160; MEDLINE-97115858; PubMed=8955160; MEDLINE-97115858; PubMed=8955160; MEDLINE-97115858; PubMed=8955160; MEDLINE-97115858; PubMed=8955160; MEDLINE-971688; PubMed=89567111; MEDLINE-971688; PubMed=89567111; MEDLINE-971688; PubMed=89567111; MEDLINE-971688; PubMed=89567111; MEDLINE-971688; PubMed=89567111; MEDLINE-971688; PubMed=8958711; MEDLINE-971688; PubMed=8958711; MEDLINE-971688; PubMed=8955160; MEDLINE-971688; PubMed=8955160; MEDLINE-971688; PubMed=8955160; MEDLINE-971688; PubMed=8955160; MEDLINE-971688; PubMed=8955160; | LT 1 PIG ST PIG ST OPMYU4; 16-OCT 2001 (Rel. 16- | 3 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 |
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| Med=10866813; L., Kittel A., g, and character rohydrolase-1."; 4106-4114(2000). Me, Sevigny J., F.H., Robson S.C. Characterization THE PREVENTION GEGULATE PURINERGJ THE PREVENTION ON ADP EQUALLY WI ND ADP EQUALLY WI ES; CALCIUM AND MI ER; DISULFIDE-LI ER; CALCIUM AND MI ER; DISULFIDE-LI ER; CALCIUM AND MI ER; DISULFIDE-LI ER; D | PRT; ad) sequence unionitation annotation diphosphd plohydroll pyrase) (() pyrase) (() pyrase) (c) | SPKD_SYNY3 GDA1_YEAST DNAK_MYCCA Y 310 HUMAN MIAA_STRPY IRX7-HUMAN VD03_VACCC VD03_VACCC VD03_VACCV VD03_VACCC VD03_VACCA AXHA_ASPNG SYK_ACICA MCCB_ARATH |
| tel A., Beaudo tel A., Beaudo tel A., Beaudo tharacterizatio se-1."; 4(2000). 14(2000). 14(2000). 14(2000). 14(2000). 14(2000). 15(1996): 22 | ; 51 ce upd tion up sphohy rolase) (CD3) (CD3 | LYEAST LYEAT L |
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A REDLINE-97115858; PubMed-8955160;
A RECEMBER E., KOZIAK K., Sevigny J., Siegel J.B., Anrather J.,
RA Beaudoln A.R., Bach F.H., Robson S.C.;
RT "Identification and characterization of CD39/vascular ATP
Identification and DTHE PREVENTION OF PLATELET AGGREGATION.
CHARACTED IN THE PREVENTION OF PLATELET AGGREGATION.
CHARACTED IN THE PREVENTION OF PLATELET AGGREGATION.
CHARACTER ATP AND ADP EQUALLY WELL.
CHARACTER REQUIRES CALCIUM AND MAGNESIUM.
CC -I- COPACTOR: REQUIRES CALCIUM AND MAGNESIUM.
CC -I- SUBUNIT: HOMODIMER; DISCUFIDE-LINKED (BY SIMILARITY).
CC -I- SUBCELULAR LOCATION: Integral membrane protein (Potential).
-I- SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                Chang A.S., Garcia R.L., Chang S.M., Schilling Submitted (MAY-1997) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5) (NTPDasel) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell activation antigen) (CD39 antigen) (Ecto-apyrase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENTPD1 OR CD39
                                                                                                                                                                                                                                                             SEQUENCE OF 97-103; 123-133; 136-140; 145-168 AND 459-471
                                                                                                                                                                                                                                                                                                                                  TISSUE-Aortic endothelium;
                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                 Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01150; GDA1_CD39; PROSITE; PS01238; GDA1_CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000407; GDA1_CD39_NTPase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  510 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium.

1 510 ECTONUCLEOSIDE TRIPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDA1_CD39_NTPASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.8%;
94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57757 MW;
                                                                                                                                                                                                                                                                                                             Chang S.M., Schilling W.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC...) (POTENTIAL)
G -> S (IN REF 2)
G -> S (IN REF 2)
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N-LINKED
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DIPHOSPHOHYDROLASE 1.
ECTOMUCLEOSIDE TRIPHOSPHATE
ECTOMOCHANGOLASE 1, 27 KDA SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred.
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                                                                                                                                                                                                                                                                                              databases.
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                                                                                                                    COULD ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
activation.";
J. Exp. Med. 185:153-163(1997).
                          "Loss of ATP diphosphohydrolase activity with endothelial cell
                                           Robson S.C., Kaczmarek E., Siegel J.B., Candinas D., Koziak K., Millan M., Hancock W.W., Bach F.H.;
                                                                            TISSUE=Umbilical vein;
MEDLINE=97149443; PubMed=8996251;
                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM VASCULAR).
MEDLINE-95015846; PDDMed=7930580;
Maliszewski C.R., Delespesse G.J.T., Schoenborn M.A., Armitage R.J.,
Fanslow W.C., Nakajima T., Baker E., Sutherland G.R., Poindexter K.,
Birks C., Alpert A., Friend D., Gimpel S.D., Gayle R. B. III;
"The CD39 lymphoid cell activation antigen. Molecular cloning and
structural characterization.";
                                                                                                                                                                                                                                                                                                                                                                       ENPI_HUMAN STANDARD; PRT; 510 AA.

P49961; Q9UQO9; Q9Y3Q9;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ectoonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
(NTPDasel) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid (NTPDasel) (Ecto-ATP diphosphohydrolase) (ATPDasel)
                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                (NYPDasel) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid activation antigen) (Ecto-apyrase) (CD39 antigen).
                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                      ENTPD1 OR CD39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                            Immunol. 153:3574-3583(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KSDTQETYGALDLGGASTQ 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS01238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           513 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDA1_CD39;
                                                                                                             (ISOFORM VASCULAR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        464 K
58113 MW;
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                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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Pred. No. 2
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INV -> CGF (IN REF. 2).
K -> V (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 513;
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                                                                                                                                                                                                                                                                                                                                                                                cell
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Titani K., Fujimura Y., Narita N.: "The cDNA cloning of human placental ecto-ATP diphosphohydrolases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97115858; PubMed-8955160;
Kaczmarek E., Koziak K., Sevigny J., Siegel J.B., Anrather
Beaudoin A.R., Bach F.H., Robson S.C.;
"Identification and characterization of CD39/vascular ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Makita K., Shimoyama T., Sakurai Y., Yagi H., Matsumoto M., Narita Sakamoto Y., Saito S., Ikeda Y., Suzuki M., Titani K., Fujimura Y.; "Placental ecto-Arp diphosphohydrolase: its structural feature distinct from CD39, localization and inhibition on shear-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 240-242; 162-166; 185-189; 210-223; 243-249 AND 288-297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matsumoto M., Sakurai Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99332082; PubMed-10405171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Christoforidis S., Papamarcaki T., Galaris D., Kellı
"purification and properties of human placental ATP
diphosphohadrolase".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEBS Lett. 453:335-340(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  platelet aggregation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diphosphohydrolase."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-30; 49-65; 94-97; 88-93; 193-223; 245-265;
                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                               EMBL; S73813; AAB32152.1; -. EMBL; U87967; AAB47572.1; -.
                                         Genew;
                                                          EMBL; AJ133133; CAB41886.1; -. EMBL; AJ133134; CAB41887.1; -.
                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein (Potential).
ALTERNATIVE PRODUCTS: 3 ISOFORMS; VASCULAR (SHOWN HERE), PLACENTAL
I AND PLACENTAL II; ARE PRODUCED BY ALTERNATIVE SPLICING.
I SUB SPECIFICITY: EXPRESSED PRIMARILY ON ACTIVATED LYMPHOID
CELLS. ALSO EXPRESSED IN ENDOTHELIAL TISSUES. THE VASCULAR ISOFORM
AND THE PLACENTAL ISOFORM II ARE PRESENT IN BOTH PLACENTA AND
UMBILICAL VEIN, WHEREAS PLACENTAL ISOFORM I IS PRESENT IN PLACENTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDES TO REGULATE PURINERGIC NEUROTRANSMISSION. CO
BE IMPLICATED IN THE PREVENTION OF PLATELET AGGREGATION.
HYDROLYZES ATP AND ADP EQUALLY WELL.
CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
COPACTOR: REQUIRES CALCIUM AND MAGNESIUM.
SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biochem. 234:66-74(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYSE ATP AND OTHER
                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY. DATABASE: NAME-PROW; NOTE-CD guide CD39 entry;
                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Hematol. 68:297-310(1998).
                                                                                                                                                                                                                                                                                                              WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd39.htm".
                     601752;
                                                                                                                                                                                                                                                                                                                                                                               .5-8.0 WITH ADP
                                      HGNC:3363; ENTPD1.
                                                                                                                                                                                                                                                                                                                                                                                                THE N-TERMINUS IS BLOCKED.
ELLANEOUS: OPTIMAL PH IS 7.0-7.5 WITH ATP AS SUBSTRATE AND
    IPR000407; GDA1_CD39_NTPase
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                                                                                                                                                                                   MEDLINE=95015846; PubMed=7930580; Maliszewski C.R., Delespesse G.J.T., Schoenborn M.A., Armitage R.J., Franslow W.C., Nakajima T., Baker E., Sutherland G.R., Poindexter K., Birks C., Alpert A., Friend D., Gimpel S.D., Gayle R.B. III; "The CD39 lymphoid cell activation antigen. Molecular cloning and structural characterization.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
(NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid (NTPDase1) (ECTO-ATP diphosphohydrolase) (ATPDASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                ENP1_MOUSE P55772;
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
                                                                "Gene structure and chromosome location of mouse Cd39 coding for an ecto-apyrase.":
                                                                                           Schoenborn M.A., Jenkins N.A., Co
Gayle R.B. III, Maliszewski C.R.;
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                      ENTPD1 OR CD39
                                                                                                                                                                                                                                                                                                                                                             activation antigen) (Ecto-apyrase) (CD39 antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 ETNNQETFGALDLGGASTQ 220
                MEDLINE=98399871; PubMed=9730622
                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KSDTQETYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                       Immunol. 153:3574-3583(1994).
HYDROLYZES ATP AND ADP EQUALLY WELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         510 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         479
500
73
                                                         Cell Genet. 81:287-289(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300
57
162
208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.18;
73.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 75; DB 1;
Pred. No. 2.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T -> TGET (IN REF. 5).
V -> Y (IN REF. 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISSING (IN ISOFORM PLACENTAL II).
SS -> G (IN REF. 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VASNEILRDPCFHPGYKKVVNVSDLYKT -> ASITQSRPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC...) (POTENTIAL)
MEDT -> MKGTKDLTSQQ (IN ISOFORM PLACENTAL
I AND ISOFORM PLACENTAL II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D -> K (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PETSAPPAPTSCCFLFQIQ (IN ISOFORM PLACENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / -> Y (IN REF. 5).
BAD87D2499649159 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                            Copeland N.G., Gilbert D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLCNAC . . .)

(GLCNAC . . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                    COULD ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                    P97687;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
(NTPDasel) (Etto-ATP diphosphohydrolase) (ATPDase) (Lymphoid (NTPDasel) (Etto-ATP diphosphohydrolase) (ATPDasel)
                                                                 Brain Res. Mol.
                                                                                                                                                                STRAIN=Sprague-Dawley; TISSUE=BraMEDLINE=96215267; PubMed=8626624;
                                                                                                  Wang T.-F., Rosenberg P.A., Guidotti G.; "Characterization of brain ecto-apyrase: evidence for only one ecto-
                                                                                                                                                                                                                               SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                        activation antigen) (Ecto-apyrase) (CD39 antigen).
                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                  ENTPD1 OR CD39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 SQKQETFGALDLGGASTQ 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: ATP + 2 H(2)0 = AMP + 2 phosphate.
-!- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM (BY SIMILARITY).
-!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-!- SUBCELULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     incerpro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 SDTQETYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L; AP037366; AAB92259 1; L; AF041818; AAC83203 1; L; AF041812; AAC83203 1; JOINED LL; AF041813; AAC83203 1; JOINED LL; AF041814; AAC83203 1; JOINED LL; AF041815; AAC83203 1; JOINED LL; AF041816; AAC83203 1; JOINED L; ARC83203 1; ARC83203 1; ARC83203 1; ARC83203 1; ARC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGI:102805; Entpd1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF041817; AAC83203.1; JOINED
                                                                                         (CD39) gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                             ; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS01238; GDA1_CD39_NTPASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            510 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium.

1 16 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                        Brain Res. 47:295-302(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDA1_CD39;
                                                                                                                                                                                                                         AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       478
499
510
73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.1%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57205 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDA1_CD39_NTPase.
                                                                                                                                                                                        TISSUE=Brain, and Hippocampus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 75;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENT IAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8E6A6113D2E13930 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             511 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                             Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                      cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                 ENP5_MESAU
                                                                                                                                                                               RESULT 6
                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                   Q9QYC8; Q9QYC9;
16-OCT-2001 (Re
16-OCT-2001 (Re
              16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CONFLICT
                                                                                                                       ENP5_MESAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U81295; AAC53195.1; EMBL; Y15685; CAA75730.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neuropharmacology 36:1189-1200(1997).

-I- FUNCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYSE ATP AND OTHER NUCLEOTIDES TO REGULATE PURINERGIC NEUROFRANSMISSION. COULD ALSO BE IMPLICATED IN THE PREVENTION OF PLATELET AGGREGATION.

HYDROLYZES ATP AND ADP EQUALLY WELL.

-I- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.

-I- COPACTOR: REQUIRES CALCIUM AND MAGNESIUM.

-I- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

-I- TISSUE SPECIFICITY: EXPRESSION OF THE PROTECTION AND ASTROCYTES,
                                                                                                                                                                                                                                                       202 SQKQATFGALDLGGSSTQ 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Sprague-Dawley; TISSUE=Bra MEDLINE=98031057; PubMed=9364474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Wistar; TISSUE-Cochlea;
MEDLINE-20050856; PubMed=10581401;
Vlajkovic S.M., Housley G.D., Greenwood D., Thorne P.R.;
"Evidence for alternative splicing of ecto-ATPase associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kegel B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            termination of purinergic transmission.";
Brain Res. Mol. Brain Res. 73:85-92(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rat brain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 432-511 FROM N.A
                                                                                                                                                                                                                                                                                                         2 SDTQETYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: N-GLYCOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ecto-ATPase and an ecto-ATP diphosphohydrolase are expressed in
                                                                                                                                                                                                                                                                                                                                                                     13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF01150; GDA1_CD39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS01238; GDA1_CD39_NTPASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR000407; GDA1_CD39_NTPase.
(Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             511 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; Antigen;
1 16 CYTOP
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIVER, MUSCLE, THYMUS, LUNG AND SPLEEN
                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57408 MW;
                                                                                                                                                                                                                                                                                                                                                                                      68.8%;
72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                   Score 66; DB 1;
Pred. No. 0.00086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cigen; Glycoprotein; Calcium; Magnesium.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4CC123D3E644C193 CRC64;
                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                           469 AA.
                                                                                                                                                                                                                                                                                                                                                                                                           Length 511;
                                                                                                                                                                                                                                                                                                                                                         Indels
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Gaps

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SEEEDS
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                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Velasco J.A., Avila M.A., Notario V.;
"The product of the cph oncogene is a truncated, nucleotide-binding protein that enhances cellular survival to stress.";
Oncogene 18:69-701(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ectonucleoside triphosphate diphosphohydrolase 5 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENTPD5 OR CD39L4 OR CPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way made the content of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99142925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EC 3.6.1.6) (NTPDase5) (Nucleoside diphosphatase) (CD39 antigen-like
                                                                                                                                                                                                                  Q9WUZ9; 0702.
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF084568; AAF22931.1; ALT_TERM.
EMBL; AF084569; AAF22932.1; .
InterPro; IPR000407; GDAL_CD39_NTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Transmembrane; Glycoprotein; Calciu
Endoplasmic reticulum; Signal; Proto-oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01238; GDA1_CD39_NTPASE; FALSE_NEG
                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence
ENTPD5 OR CD39L4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 SQETMGTLDLGGASTO 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 TQETYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLYCOPROTEINS FOLDING AND QUALITY CONTROL IN THE ENDOPLASMIC RETICULUM. HYDROLYZES UDP, GDP AND IDP BUT NOT ANY OTHER NUCLEOSIDE DI-, MONO- OR TRIPHOSPHATES, NOR THIAMINE PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COFACTOR: REQUIRES CALCIUM AND MAGNESIUM (BY SIMILARITY). SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: LIKELY TO PROMOTE REGLYCOSYLATION REACTIONS INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUES.
DISEASE: CPH ONCOGENE HAS TRANSFORMING CAPACITY AND TUMORIGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBLELLULAK LOCATION: Endoplasmic reticulum lumen (By similarity).
TISSUE SPECIFICITY: EXPRESSED IN FETAL CELLS AND MOST ADULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleotide + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)0 = a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY)
                                     (ER-UDPase)
                                                                                                                                                                                                                                                                                                          MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF01150; GDA1_CD39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                        070214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      469 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Proto-oncogene cph).
                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=9989819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52125 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.0012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIPHOSPHOHYDROLASE 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECTONUCLEOSIDE TRIPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03D8A23E0C73474B CRC64;
                                                                                                                                                                                                                                                                                                                      427 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Calcium; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Raito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Raito T., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kandya M., Lee N.H.,
RA Lyons P., Marchhomi L., Mashima J., Mazzarelli J., Mombaetts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Havyashaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Kidney;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           endoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Glycoprotein reglucosylation and nucleotide sugar utilization in the secretory pathway: identification of a nucleoside diphosphatase in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chadwick B.P., Williamson J., Sheer D., Frischauf A.-M.; "CDNA cloning and chromosomal mapping of a mouse gene with homology to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBO J. 18:3282-3292(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99298181; PubMed=10369669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mamm. Genome 9:162-164(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98119025; PubMed=9457681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:585-590(2001).
-i- FUNCTION: LIKELY TO PROMOTE BEGIVENOCUTETY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                          -!- MISCELLANEOUS: OPTIMAL PH IS NEUTRAL.
-!- SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                            -!- PTM: GLYCOSYLATED WITH HIGH MANNOSE N-LINKED GLYCANS.
                                                                                                                                                                                                                                                                                                                                                                                                                     -!- TISSUE SPECIFICITY: UBIQUITOUS
                                                                                          EMBL; AJ238636;
                                                                                                                 EMBL; AF006482; AAC05181.1; -.
                         MGD; MGI:1321385; Entpd5.
InterPro; IPR000407; GDA1_CD39_NTPase.
                                                                 EMBL; AK002618; BAB22234.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleotide + phosphate.
COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)0 - a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLYCOPROTEINS FOLDING AND QUALITY CONTROL IN THE ENDOPLASMIC RETICULUM. HYDROLYZES UDP, GDP AND IDP BUT NOT ANY OTHER NUCLEOSIDE DI-, MONO- OR TRIPHOSPHATES, NOR THIAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: LIKELY TO PROMOTE REGLYCOSYLATION REACTIONS INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYROPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helenius A.
                                                                                             CAB45533.1;
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Pfam; PF01150; GDA1_CD39; 1.

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RESULT 8
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                                                  Pfam; PF01150; GDA1_CD39; 1.
                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                           Genew; HGNC:3367; ENTPD5
MIM; 603162; -.
                                                                                                                                                                                                                                                                                                                                                                                                              -i- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
-i- TISSUE SPECIFICITY: EXPRESSED IN ADULT LIVER, KIDNEY, PROSTATE,
TESTIS AND COLON. MUCH WEAKER EXPRESSION IN OTHER TISSUES.
-i- SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
                                                                 InterPro; IPR000407; GDA1_CD39_NTPase.
                                                                                                                                                       EMBL; AF039918; AAC39885.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIJINE=98341119; PubMed=9676430; Chadwick B.P., Frischauf A.-M.;
"The CD39-like gene family: identification of three new human members (CD39L2, CD39L3, and CD39L4), their murine homologues, and a member of the gene family from Drosophila melanogaster.";
Genomics 50:357-367(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        075356;
16-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 5 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENTPD5 OR CD39L4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENP5_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 QETVGTLDLGGASTQ 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleotide + phosphate.
COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: LIKELY TO PROMOTE REGLYCOSYLATION REACTIONS INVOLVED IN GLYCOPROTEINS FOLDING AND QUALITY CONTROL IN THE ENDOPLASMIC RETICULUM. HYDROLYZES UDP, GDP AND IDP BUT NOT ANY OTHER NUCLEOSLIDE DI, MONO- OR TRIPHOSPHATES, NOR THIAMINE PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 QETYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)0 = a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.6.1.6) (NTPDase5) (Nucleoside diphosphatase) (CD39 antigen-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPOO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301238; GDA1_CD39_NTPASE; FALSE_NEG. Transmembrane; Glycoprotein; Calcium; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISEPVFSQEGVDSETFSDLSGKAWPETR (IN REF. 1).
2F9DA2C342C55577 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIPHOSPHOHYDROLASE 5.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLTAHKESEQHRDWLGLGGHLSPAPVSGHHQLRPSSTSEAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECTONUCLEOSIDE TRIPHOSPHATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.
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has 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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                             ACCEPTER A A RANGER AND RANGER AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENP3
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WUTAGENESIS OF R-67; R-143; R-146; E-182; N-191; S-224 AND Q-226. MRDLINE-21197753; PubMed=11300774; Yang F., Hicks-Berger C.A., Smith T.M., Kirley T.L.; "Site-directed mutagenesis of human nucleoside triphosphate diphosphohydrolase 3; the importance of residues in the apyrase conserved regions."; Blochemistry 40:3943-3950(2001).
                                                                                                                                                                                                                                                                                                         ATPases: inactivation and conversion of an ecto-apyrase to an
                                                                                                                                                                                                                                                                                                                                                                 MUTAGENESIS OF TRP-187; ASP-219 AND TRP-459.
MEDLINE-99249795; PubMed-10231536;
Smith T.M., Lewis Carl S.A., Kirley T.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chadwick B.P., Frischauf A.-M.;
"The CD39-like gene family: identification of three new human members (CD3912, CD3913, and CD3914), their murine homologues, and a member of the gene family from Drosophila melanogaster.";
Genomics 50:357-367(1998).
                                                                                                                                                                                                                                                               Biochemistry 38:5849-5857(1999).
                                                                                                                                                                                                                                                                                                   ecto-NTPase."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith T.M., Kirley T.L.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning, sequencing, and expression of a human brain ecto-apyrase related to both the ecto-ATPases and CD39 ecto-apyrases."; Biochim. Biophys. Acta 1386:65-78(1998).
                                                                                                                                                                                                                                                                                                                                    "Mutagenesis of two conserved tryptophan residues of the E-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENP3_HUMAN STANDARD; PRT; 529 AA.
075355; 060495;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 3 (EC 3.6.1.5)
(NTPDase3) (Ecto-ATP diphosphohydrolase) (ATPDase) (Ecto-apyrase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith T.M., Kirley T.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98342144; PubMed=9675246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Keratinocytes;
MEDLINE=98341119; PubMed=9676430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CD39 antigen-like 3) (HB6).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01238; GDA1_CD39_NTPASE; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 QETVGTLDLGGASTQ 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                368
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Pred. No. 0.0016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIPHOSPHOHYDROLASE 5
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B Q

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-I- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
-I- COPACTOR: REQUIRES CALCIUM AND MAGNESIUM.
-I- SUBCELLIDAR LOCATION: Integral membrane protein (Potential).
-I- TISSUE SPECIFICITY: EXPRESSED IN ADDUT BRAIN, PANCREAS, SPLEEN AND PROSTATE. MODERATE OR LOW EXPRESSION IS SEEN IN MOST TISSUES. NOT EXPRESSED IN LIVER AND PERIPHERAL BLOOD LEUKOCYTES.
-I- SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF039917; AAC39884.1; -. EMBL; AF034840; AAC09236.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 603161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                             ENP1_CHICK 093295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01238; GDA1_CD39_NTPASE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000407; GDA1_CD39_NTPase.
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                          213 ETTGALDLGGASTQ 226
                                                                                                                                                                                                                                                                                           6 ETYGALDLGGASTQ 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGNC:3365; ENTPD3
                                                                                                                                                                                                                                                                                                                                                                        Similarity
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529 AA;
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                                                                                                                                                                                                                                                                                                                                                  Conservative
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191
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                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                        64.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Calcium; Magnesium.
CYTOPLASMIC (POTENTIAL).
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N-LINKED (GLCNAC...) (POTENTIAL).
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N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                               Score 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE ATP HYDROLYSIS. V -> A (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R->P: INCREASE OF ATPASE ACTIVITY,
DECREASE OF ADPASE ACTIVITY.
                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                  Mismatches
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COMPLETE LOSS OF ACTIVITY.

LOSS OF ACTIVITY.

INCREASE OF ACTIVITY, ESPECIALLY
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COMPLETE LOSS OF ACTIVITY.
COMPLETE LOSS OF ACTIVITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INCREASE OF ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 529;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 272:236445-23652(1997).

J. Biol. Chem. 272:23645-23652(1997).

J. Biol. Chem. 272:23645-23652(1997).

J. Biol. Chem. 272:23645-23652(1997).

J. Biol. Chem. 272:23645-23652(1997).

J. Biol. Chem. 272:23652(1997).

J. BIOL. Chem. 272:23652(1997).

BE IMPLICATED IN THE PREVENTION OF PLATELET AGGREGATION.

BE IMPLICATED IN THE PREVENTION OF PLATELET AGGREGATION.

BE IMPLICATED IN THE PREVENTION OF PLATELET AGGREGATION.

HYDROLYZES ATP AND ADD EQUALLY WELL (BY SIMILARITY).

-I- CATALYTIC ACTULTY: ATP + 2 H(2)0 = AMP + 2 phosphate.

-I- COPACTOR: REQUIRES CALCIUM AND MAGNESIUM (BY SIMILARITY).

-I- SUBBUNIT: HOMODIMER; DISULFIDE-LINKED (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nagy A.K., Knowles A.F., Nagami G.T.;
"MoLecular cloning of the chicken oviduct ecto-ATP-diphosphohydrolase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lewis-Carl S., Kirley T.L.; "Immunolocalization of the ecto-ATPase and ecto-apyrase in chicken gizzard and stomach. Purification and N-terminal sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97442428; PubMed=9295305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98298108; PubMed=9632655;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PTM: N-GLYCOSYLATED.
-!- SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                   CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
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                                                                                                 SEQUENCE
                                                                                                                                                       CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pro; IPR000407; GDA1_CD39_NTPase. PF01150; GDA1_CD39; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS01238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium.

1 7 CYTOPLASMIC (POTENTIAL).
                                                                                                 493 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDA1_CD39_NTPASE; 1.
                      60.4%;
85.7%;
                      Score 58; DB 1;
Pred. No. 0.021;
                                                                                                                                I -> G (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
                                                                                                                                                  C -> W (IN REF.
                                                                                                                                                                           N-LINKED (GLCNAC
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                                                                                                                                                                                                                                                         N-LINKED
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                                                                                                                                                                                                                                                                                                                  N-LINKED
                                                                                                 -> G (IN REF. 1; AA SEQUENCE).
F14FF4C3AA2F3603 CRC64;
                                                                                                                                                                                                                                                              (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC . . .)
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                                                Length 493
                                                                                                                                                                                                                                                                                           (POTENTIAL).
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CARBOHYD CARBOHYD

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Matches

SEQUENCE

CONFLICT

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                           DOMAIN
                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U91510; AAB81013.1; -. EMBL; AF144748; AAD40239.1; -.
                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                             Pfam; PF01150;
                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                     PROSITE; PS01238; GDA1_CD39_NTPASE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                      RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (LONG FORM), AND CHARACTERIZATION. MEDLINE-99441286; PubMed=10510450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mateo J., Harden T.K., Boyer J.L., "Functional expression of a CDNA encoding a human ecto-ATPase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chadwick B.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Keratinocytes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENTPD2 OR CD39L1
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 2 (EC 3.6.1.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97419269; PubMed=9271669;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning and mapping of a human and mouse gene with homology to ecto-\Upsilon Pase genes.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (SHORT FORM).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9Y5L3; 015464;
                                                                                                                                                                                                  ternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NTPDase2) (Ecto-ATPase) (CD39 antigen-like 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDES TO REGULATE PURINERGIC NEUROTRANSMISSION. HYDROLYZES ADP ONLY TO A MARGINAL EXTENT. THE ORDER OF ACTIVITY WITH DIFFERENT SUBSTRATES IS ATP > GTP > CTP = ITP > UTP >> ADP = UDP. CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate. COFACTOR: REQUIRES CALCIUM AND MAGNESIUM. SUBCELLULAR LOCATION: Integral membrane protein (Potential). ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. TISSUE SPECIFICITY: BRAIN, PLACENTA, SKELETAL MUSCLE, KIDNEY, TISSUE SPECIFICITY: BRAIN, PLACENTA, SKELETAL MUSCLE, KIDNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PANCREAS, HEART, OVARY, TESTIS, COLÓN, SMALL INTESTINE, PROSTATE AND PANCREAS. NO EXPRESSION IN ADULT THYMUS, SPLEEN, LUNG, LIVER AND PERIPHERAL BLOOD LEGKOCYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Pharmacol. 128:396-402(1999).
FUNCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYZE ATP AND OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 ETYGALDLGGASTQ 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome 8:668-672(1997).
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                                                                                                                                                                                                                                                                                                                                                                                 HGNC:3364; ENTPD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Conservative
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                                                                                                                                                                                                                                                                                          splicing.
                                                                                                                                                                                                            Transmembrane; Glycoprotein; Calcium; Magnesium;
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484
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                                        462
483
495
                          CYTOPLASMIC (POTENTIAL)
                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                       EXTRACELLULAR (POTENTIAL).
                                                                   POTENTIAL
                                                                                                                        POTENTIAL.
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             DITION OF THE PROPERTY OF THE 
                                                                                                                                         RA Kawai J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
R Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml I.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Nordone P., King B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Havashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                       Nature 409:685-690(2001).
                                                                                          "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                  Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (LONG FORM).
STRAIN-C57BL/6J; TISSUE-Kidney;
MEDLINE-21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression.
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 2 (EC 3.6.1.3)
ENTPD2 OR CD3911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A novel response to dioxin. Induction of ecto-ATPase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98288263; PubMed=9624117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATPase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97419269; PubMed=9271669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (SHORT FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning and mapping of a human and mouse gene with homology to ecto-
ATPase genes ":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Embryo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem.
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NUCLEOTIDES TO REGULATE PURINERGIC NEUROTRANSMISSION. HYDROLYZES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome 8:668-672(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dong L., Whitlock J.P. Jr.;
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129
294
378
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383
495 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273:15358-15365(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53665 MW;
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MISSING (IN SHORT ISOFORM).
MISSING (IN SHORT ISOFORM).
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Pred. No. 0.046;
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VARSPLIC
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                                                                                                                                                                                                                                                                                                     035795; 09JHY5; 09WVE7;
16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 2 (EC 3.6.1.3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01150;
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Pfam; PF01150; GDA1_CD39; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
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                                                                                                                                                                                                                                                  (NTPDase2) (Ecto-ATPase) (CD39 antigen-like 1). ENTPD2 OR CD39L1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          ENP2_RAT
                             STRAIN-Sprague-Dawley; TISSUE-Brain; MEDLINE-98031057; PubMed-9364474;
                                                                                  SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION
                                                                                                                                        NCBI_TaxID=10116
                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                           Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 TLGAMDLGGASTO 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADP ONLY TO A MARGINAL EXTENT (BY SIMILARITY).
CATALYTIC ACTIVITY: ATP + H(2)0 = ADP + phosphate.
COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 TYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDUCTION: BY DIOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Integral membrane protein (Potential). ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF042811; AAC24347.1; -.; AK002553; BAB22182.1; -. MGI:1096863; Entpd2.
  B., Braun N., Heine P., Maliszewski C.R., Zimmermann H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAS PROBABLY DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane; Glycoprotein; Calcium; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            484
64
129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54310 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC...) (PUTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 56; DB 1;
Pred. No. 0.046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                495 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Evidence for alternative splicing of ecto-ATPase associated with termination of purinergic transmission."; brain Res. Mol. Brain Res. 73:85-92(1999).

FINCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYZE ATP AND OTHER NUCLEOTIDES TO REGULATE PURINERGIC NEUROTRANSMISSION. HYDROLYZES ADP ONLY TO A MARGINAL EXTENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "An ecto-ATPase and an ecto-ATP diphosphohydrolase are expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Sprague-Dawley; TISSUE=Sert MEDLINE=21121474; PubMed=11229804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rat brain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, HEART, VAS DEFERENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuropharmacology 36:1189-1200(1997).
                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- INDUCTION: BY FSH IN SERTOLI CELLS BUT NOT IN PERITUBULAR CELLS;
BY CAMP IN BOTH TYPE OF CELLS.
-!- PTM: HAS PROBABLY DISULFIDE BONDS.
-!- SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vlajkovic S.M., Housley G.D., Greenwood D., Thorne P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Wistar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lu Q., Porter L.D., Cui X., Sanborn B.M.;
"Ecto-ATPase mRNA is regulated by FSH in Sertoli cells.";
                                                                                                                                                                                                                                                                                                                                                                                           Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               FIGHT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Y11835; CAA72533.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20050856; PubMed=10581401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 379-495 FROM N.A. (ISOFORM 2).
                                                   SEQUENCE
                                                                                                                                                                                                        CARBOHYD
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                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                    CONFLICT
                                                                                      CONFLICT
                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Androl. 22:289-301(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.
SUBCELLULAR LOCATION: Integral membrane protein (Potential).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2: ARE
PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF276940; AAF87740.1; -. AF129103; AAD42303.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                               PF01150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR000407;
                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane; Glycoprotein; Calcium; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKELETAL MUSCLE, THYMUS, LUNG AND SPLEEN. WEAK EXPRESSION
                                                   495 AA;
                                                                                                                                                                                                        463
484
129
1294
294
306
319
378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Cochlea
                                                                                                                                                                                                                                                                                                                                                                                                                                                GDA1_CD39
                                                       54389 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDA1_CD39_NTPase
   58.3%; Score 56; DB 1; 84.6%; Pred. No. 0.046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Sertoli cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sanborn B.M.;
                                                                                                                                                                                                                              N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                      A -> T (IN REF. 2).
L -> F (IN REF. 2).
                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                    Score 56;
                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL)
                                                                                                         PF -> LL (IN REF.
                                                                                                                                                          FLSGPLERQAPEPTGWESVPCLLVKTFVIKDFS (IN
                                                                                                                                                                           VRSAKSPGAL
                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                       T -> A (IN REF.
                                                                                                                                        ISOFORM 2)
                                                         237B999F1BEB8E00 CRC64;
                    DB 1;
                                                                                                                                                                           -> DVRSQPVTQGEVHSEWDFCSDLQGPGN
                      Length 495;
                                                                                                       2)
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RESULT 14
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                  CONFLICT
                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EMPL on the EMPL of Bioinformatics are no restrictions on its modified and this statement is not removed. Usage by and for commercial
                                                      CARBOHYL
                                                                    CARBOHYD
                                                                                    CARBOHYD
                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                    DOMAIN
                                                                                                                     DOMAIN
                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                               EMBL; U74467; AAC60071.1;
                                                                                                                                                   DOMAIN
                                                                                                                                                                                                    INIT_MET
                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Purification and characterization of the ecto-Mg-ATPase of chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-12 AND 154-176, AND CHARACTERIZATION. MEDILINE-95081479; PubMed-7989647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATPase. Homology with the lymphoid J. Biol. Chem. 272:1076-1081(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144-150; 154-176; 208-217; 25
383-389; 448-456 AND 459-479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 1-21; 68-73; 83-90; 108; 121; 144-150; 154-176; 208-217; 251-258; 273-284; 337-352; 374-380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 2 (EC 3.6.1.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97150869; PubMed=8995405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Skeletal muscle, and Gizzard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENTPD2 OR CD39L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complementary DNA cloning and sequencing of the chicken muscle ecto-
TPase: Homology with the lymphoid cell activation antigen CD39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NTPDase2) (Ecto-ATPase) (CD39 antigen-like 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENP2_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 TLGAMDLGGASTQ 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 TYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDES TO REGULATE PURINERGIC NEUROTRANSMISSION. HYDROLYZES ADP ONLY TO A MARGINAL EXTENT (BY SIMILARITY).
CATALYTIC ACTIVITY: ATP + H(2)0 = ADP + phosphate.
COPACTOR: REQUIRES CALCIUM AND MAGNESIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Integral membrane protein (Potential). PTM: HAS PROBABLY DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION:
                                                                                                                                                                                                      PE; PS01238; GDA1_CD39_NTPASE; 1.
Lase; Transmembrane; Glycoprotein; Calcium; Magnesium.
                                                                                                                                                                                                                                             PF01150; GDA1_CD39_NTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J.G., Kirley T.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 smooth muscle."
                61
296
417
443
                                                                                               4 6 5 5
8 6 5 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        iophys. Methods 29:61-75(1994).
IN THE NERVOUS SYSTEM, COULD HYDROLYZE ATP AND OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
 N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
L -> LL (IN REF. 2).
                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.
                                                                                               POLY-LEU.
                                                                                                                                        EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              494 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : SQ
   Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YND1_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local
                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/
                                             Pfam; PF01150; GDA1_CD39; 1.
PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
     TRANSMEM
                       DOMAIN
                              Hydrolase; Transmembrane; Golgi stack.
                                                                                               EMBL; AF203695; AAF17573.1; -. SGD; S0000807; YND1.
                                                                                                                                 EMBL; U18778; AAB64538.1; -.
                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P40009;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Golgi apyrase (EC 3.6.1.5) (ATP-diphosphatase) (Adenosine
diphosphatase) (ADPase) (ATP-diphosphohydrolase) (Golgi nucleoside
                                                                               InterPro; IPR000407; GDA1_CD39_NTPase
                                                                                                                                                                                                                               the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99340091; PubMed=10409709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YND1 OR YER005W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YND1_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 KKTLGAMDFGGASTQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 QETYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   494 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
   500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54402 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.2%;
66.7%;
POTENTIAL
              LUMENAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 54; DB 1; Length 494; Pred. No. 0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENF -> GNK (IN REF. 2).
; 1E0E0E631DA621EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  630 AA
                                                                                                                                                                                                             There are no restrictions on ong as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cherry J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
                                                                                                                                                                            Result
                                                                                                                                                                                                                                                                                                                                                                                                                              Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                   ö
                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-781-796B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   February 11, 2003, 18:33:31; Search time 92 Seconds
                                                                                                                                                                   Match Length DB ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KSDTQETYGALDLGGASTQ 19
                                                                                                                                                                              Query
78.1
666.7
660.4
660.4
560.3
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581.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                         sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                               sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                  sp_archea:*
                                                                                                                                                                                                                                                                                                                                                sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                         sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                      sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                             sp_invertebrate:*
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sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                             sp_virus:*
sp_vertebrate:*
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                                                                                                                                                                                                                                                                                                                           sp_plant:*
                                                                                                                                                11 Q921Q6
                                                                                                                                      4 Q8WUB3
                                                                0 049676
Q9UT35
                                                                                                                            Q96RX0
                                                                                               Q8S613
Q921R1
                             Q9X162
Q9FUI1
Q8R0U1
Q9XFC9
                                                                                                                    Q90x66
          Q8RVT6
                    Q8S7F1
                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.553 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (without alignments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       671580
                                                                                     Q90x66 gallus gall
Q8s6i3 oryza sativ
Q921r1 mus musculu
Q9d813 mus musculu
                                                                   Q9ut35 schizosacch
                                                                                                                            Q8wub3 homo sapien
Q96rx0 homo sapien
                                                                                                                                                                    Description
                                               Q9xi62 arabidopsis
Q9fuil pisum sativ
                   Q8s7f1
                                                                             049676 arabidopsis
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Q921Q6
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| 43 | 43 | 43 | 43 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44.5 | 45 | 46 | 46 | 46 | 46.5 | 46.5 | 47 |
| 44.8 | 44.8 | 44.8 | 44.8 | 45.8 | 45.8 | 45.8 | 45.8 | 45.8 | 45.8 | 45.8 | 45.8 | 45.8 | 45.8 | 45.8 | 45.8 | 45.8 | 45.8 | 45.8 | 45.8 | 45.8 | 46.4 | 46.9 | 47.9 | 47.9 | 47.9 | 48.4 | 48.4 | 49.0 |
| 494 | 468 | 456 | 313 | 2225 | 2139 | 925 | 555 | 555 | 473 | 472 | 472 | 471 | 464 | 461 | 455 | 455 | 455 | 447 | 407 | 405 | 326 | 476 | 550 | 483 | 148 | 604 | 572 | 690 |
| 16 | 10 | 10 | 16 | ŗσ | ω | 12 | 10 | 10 | 10 | 10 | 10 | 10 | σ. | 5 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | N | 4 | 4 | 10 | 4 | w | σ |
| Q9RB68 | Q9FVC2 | 09SPM8 | Q9F2Q6 | Q9VJ82 | Q9P880 | Q69138 | 080612 | Q94EZ2 | Q8RVT8 | Q9SPM5 | Q9M7B3 | Q9SQG2 | Q9VQI8 | 076268 | Q8RVT9 | Q8RVU0 | Q9FEA6 | Q9SLV4 | 8NAV6Ö | Q9M9T7 | Q9AU14 | Q9RQ11 | Q9NTN2 | Q8TAS7 | Q9xGR6 | Q9NQZ7 | Q9USP2 | о9вну5 |
| Q9rb68 chlamydia p | | | | Q9vj82 drosophila | Q9p880 botrytis ci | 8 | | | | | | | Ω | | 10 | pisum | pisum | pisum | pisum | | 4 | Q9rqll bacteroides | | homo | Q9xgr6 xanthoceras | ' 2 | | Q9bhv5 leishmania |

ALIGNMENTS

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Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                    Matches
                                                                         Q8WUB3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC011278; AAH11278.1;...
InterPro; IPR000407; GDAL_CD39_NTPase.
Pfam; PF01150; GDAL_CD39; 1.
PROSITE; PS01238; GDAL_CD39_NTPASE; UNKNOWN_1.
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TREMBLrel. 19, Created)
01-DEC-2001 (TREMBLRel. 19, Last sequence update)
01-DEC-2002 (TREMBLRel. 21, Last annotation update)
Similar to ectonucleoside triphosphate diphosphohydrolase 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q921Q6
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                     202 SQKQETFGALDLGGASTQ 219
                                                                                                                                                                                                                                                                                                                                         Match 78.1%; Score 75; DB 11; Length 510; Local Similarity 83.3%; Pred. No. 0.00028;
                                                                                                                                                                                                                                                                     2 SDTQETYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                       15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      510 AA; 57176 MW; E77BB644AE1413A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                         407 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         510 AA.
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096RX0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Ecto-ATP-diphosphohydrolase (EC 3.61.5).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           NCBI_TaxID=9031;
                                                              Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                              Q90x66;
                                                                                                                                                                                                                                                                                        Q90X66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ol-DEC-2001 (TrEMBLrel. 19, Created)
Ol-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Ol-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000407; GDA1_CD39_NTPase.
Pfam; PF01150; GDA1_CD39; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Carcinog. 27:229-236(2000).
EMBL; AF136572; AAK82950.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      structure, chromosomal mapping, and expression in normal and tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The human PCPH proto-oncogene: cDNA identification, primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=20173601; PubMed=10708485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pcph proto-oncogene protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q96RX0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases EMBL; BC020966; AAH20966.1; -. InterPro; IPR000407; GDAL_CD39, NTPase. Pfam; PF01150; GDA1_CD39; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recio J.A., Zambrano N., Pena, Ld, Reig J.A., Rhoads A., Rouzaut A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q96RX0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                           192 QETVGTLDLGGASTQ 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similar to ectonucleoside triphosphate diphosphohydrolase 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 QETVGTLDLGGASTQ 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 QETYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       428 AA; 47431 MW; F2C4F7DE650A44F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       407 AA; 45336 MW;
                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%; Score 64; 86.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.7%;
86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.018;
                                                                                                                                                                                                                                                                                   PRT;
                                                        Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D92A5F7DC9EC9E5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                   493 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                428 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
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RN OCC OCC
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                                                                                                                                                                                                                                                                                                                               Q921R1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MCCombie W.R., de la Bastide M., Spiegel L., Preston R., Kirchoff K., Kuit K., Nascimento L., Baker J., Santos L., Zutavern T., Miller B., Cunnius D.M., Katzenberger F., Muller S., Bell M., Balija V., Shah R., King L., Yang C., Dike S., O'Shaughnessy A., Palmer L., Dedhia N.; "Genomic sequence for Oryza sativa, Nipponbare strain, clone OSJNBD0023M11, from chromosome 10, complete sequence."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                       Mus musculus (Mouse)
                                                                                                                                        ENTPD2
                                                                                                                                                                                                                                                                       Q921R1;
                                                                                                                                                                                                                                                                                                 Q921R1
                    NCBI_TaxID=10090;
                                                                                                                                                         Ectonucleoside triphosphate diphosphohydrolase 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridipiantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8S6I3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Putative nucleoside phosphatase. OSJNBB0023M11.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF426405; AAL25086.1; -.
Interpro; IPR000407; GDA1_CD39_NTPase.
Pfam; PF01150; GDA1_CD39; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Knowles A.F., Nagy A.K., Strobel R.S., Wu-Weis M.; "Purification, molecular cloning, and expression of the chicken liver ecto-ATP-diphosphohydrolase.", Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                 260 SSSKMTYGSLDLGGSSLQ 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 EVLGALDLGGASTQ 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 SDTQETYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 ETYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS01238; GDA1_CD39_NTPASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     681 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              493 AA; 54063 MW; 0380449E86167B70 CRC64;
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                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75002 MW; B1E87479202580BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.4%; Score 61.1%; Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.4%; Score 58; DB 1 85.7%; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches

 Mismatches

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Pred. No. 0.32;
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                                                                                                                                                                                                                                                                                                 495 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       681 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 681;
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RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrimi L.M., Stabbli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schrimi L.M., Stabbli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Hoyons P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Worshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Havashiraki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Havashiraki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                         Matches
                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011241; AAH11241.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01238; GDA1_CD39_NTPASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-C57BL/6J; TISSUE-SMALL INTESTINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9D813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1096863; Entpd2.
InterPro; IPR000407; GDA1_CD39_NTPase.
                                                                                                                                                                              MGD; MGI:1919340; 2010320H07Rik.
InterPro; IPRO00407; GDA1_CD39_NTPASE.
Pfam; PF01150; GDA1_CD39; 1.
SEQUENCE 300 AA; 33646 MW; CCDE372AF12C6B16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2010320H07RIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2010320H07Rik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196 TLGAMDLGGASTQ 208
                                                                                                                                                                                                                                                                                         Nature 409:685-690(200)
                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 TYGALDLGGASTQ 19
                                                                                                             Local Similarity
                                           9 GALDLGGASTQ 19
GALDLGGASTQ 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF01150; GDA1_CD39;
                                                                                                                                                                                                                                                                        AK008590; BAB25764.1; -
                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        495 AA; 54319 MW; A76468A0CBF86AAC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                         Conservative
                                                                                       56.2%; Score 54; DB 11; Length 300; 100.0%; Pred. No. 0.58; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 56; DB 11; Length 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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RESULT 8

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049676
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Q9UT35
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical 116.4 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantaa; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   049676
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                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative guanosine-diphosphatase (Guanosine diphosphatase).
SPAC824.08 OR GDP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUM Arabidopsis sequencing project; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases EMBL; AL021887; CAA16707.1; -. EMBL; AL161550; CAB78920.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bevan M., Benes V., Rechmann S., Borkova D., Ansorge W., Bancroft I., Mewes H.W., Mayer K., Schueller C.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. SEQUENCE 1052 AA; 116388 MW; 88C4AF1F16225987 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                   Q9UT35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01150; GDA1_CD39; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00892; DUF6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000620; DUF6.
InterPro; IPR000407; GDA1_CD39_NTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
            Schizosaccharomyces pombe.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL12174; CABS7388 1; ...
EMBL; AF465240; AAL69974 1; ...
                                                                              Sanchez R., Franco A., Notario V., Gacto M., Cansado J., "Characterization of a guanosine diphosphatase gene from
                                                                                                                                                                                STRAIN-972H-;
                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                  Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                     Q9UT35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     685 TFGALDLGGSSLQ 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                 Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                     Schizosaccharomyces.
InterPro; IPR000407; GDA1_CD39_NTPase.
                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 TYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rechmann S., Borkova D., Ansorge W., Mewes H.W., Lemcke K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                ., Rajandream M.A., Quail M., Seegar K., Harris D.;
                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.2%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 53; DB 10; Length 1052;
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                                                                                                                                                                                                                                                                                        Schizosaccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                         556 AA.
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P SEQUENCE FRUM N...

(C STRAIN-CV. COLUMBIA)

(C STRAIN-CV. COLUMBIA)

(A Federapiel N. A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,

RA Federapiel N. A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,

RA Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,

Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,

RA Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,

RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

DR EMBL, AC007576, AAD39311 1.

DR InterPro; IPR000407; GDA1_CD39_NTPASE.

DR InterPro; IPR000407; GDA1_CD39_NTPASE.

DR PROSITE; PS01238; GDA1_CD39_NTPASE; UNKNOWN_1.

PROSITE; PS01238; GDA1_CD39_HBLIX; UNKNOWN_1.

SEQUENCE 483 AA; 53425 MW; 4E31D13830F1C8F9 CRC64;
                 B
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Q9XI62
                                                                                                                                                                                                                                                           Q9FUI1
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
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SQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                       Jin L., Roux S.J.; "Cloning of a Second Apyrase in Pisum sativum."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ da
            EMBL; AF305783; AAG22044.1; -.
                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicleae; Pisum.
                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                  SEQUENCE FROM N.A.
                                                                                                                                          Pisum sativum (Garden pea)
                                                                                          NCBI_TaxID=3888;
                                                                                                                                                                          Apyrase 2.
                                                                                                                                                                                                                                            Q9FUI1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01150; GDA1_CD39; 1.
PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
SEQUENCE 556 AA; 61588 MW; 1D811E3D6A6BBB85 CRC64;
                                                                                                                                                                                                                                                                                                           212 TDPLETTGIVELGGASAQ 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F7A19.34 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9XI62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 THSTVAVMDLGGASTQ 291
                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                     2 SDTQETYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 TQETYGALDLGGASTQ 19
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                                                                                                                                                                                                                                         PRELIMINARY;
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55.6%;
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62.5%;
                  the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                       PRT;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                        447 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DE OS OC OC OC OX RN RP RC RA RA FT
     RESULT 13
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     SEQUENCE
               Hydrolase;
                                                                                Proc. Natl.
                                                                                               roots.
                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                     NCBI_TaxID=3840;
                                                                                                                                                                                                                                                                                                                                                       Q9xFC9
                                                                                                                                                                                                                                                                                                                                          Q9XFC9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8R0U1
                                                                                                                                                                                                                                                                                                                                                                                                                    107 KRTAGVLDMGGVSTQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8R0U1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01238; GDA1_CD39_NT
SEQUENCE 447 AA; 48783 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 DYSDTVGVVDLGGGSVQ 203
                                                                                                                                                                                                                                                                                                                                                                                                                                               5 QETYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity es 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 DTQETYGALDLGGASTQ 19
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462 AA; 51183 MW; 59F865A9D4CC444B CRC64;
                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.0%;
52.9%;
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EMBL; AF139807; AAD31285.1; -. InterPro; IPR000407; GDA1_CD39_NTPase. Pfam; PF01150; GDA1_CD39; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                          Dolichos biflorus (Horse gram)
Eukaryota; Viridiplantae; Strep
                                                                                                                                                                                     Etzler M.E., Kalsi G., Ewing N.N., Roberts N.J., Day R.B.,
Murphy J.B.;
                                                                                                                                                                                                                                 MEDLINE=99254131; PubMed=10318974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nod factor binding lectin-nucleotide phosphohydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to lysosomal apyrase-like 1 (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000407; GDA1_CD39_NTPase.
Pfam; PF01150; GDA1_CD39; 1.
                                                                                                                                                    factor binding lectin with apyrase activity from legume
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  448 AA; 51285 MW; 0DA76F8BA734E3D6 CRC64;
                                                                                                     Acad. Sci. U.S.A. 96:5856-5861(1999)
                                                                                                                                                                                                                                                                                                                                                           Fabales; Fabaceae; Papilionoideae; Phaseoleae; Dolichos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _CD39_NTPASE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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Pred. No. 10;
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Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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Best Local Similarity 52.9%;
Matches 9; Conservative
                Query Match 49.0%; Score 47; DB 10; Length 467; Best Local Similarity 52.9%; Pred. No. 16;
   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN-CV NIPPONIARE;

Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,

Buell C.R., Yuan Q., Ouyang S., Hance M., Shvartsbeyn M.,

Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G.,

VanAken S. E., Utterback T. R., Feldblyum T.V., Kalb E., Ouackenbush J.,

Salzberg S.L., White O., Fraser C.M.;

Oryza sativa chromosome 3 BAC OSJMBbO04BD20 genomic sequence.";

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AC084766; AAL82534.1;

EMBL; AC084766; AAL82534.1;

SEQUENCE 635 AA; 69757 MW; 61E3F7BODIEA4913 CRC64;
                                                                                           Kawahara T., Miura A., Kiba A., Toyoda K., Ichinose Y., Shiraishi T., "Characterization of Pea Cell Wall-bound Apyrase."; "Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza. NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                EMBL; AB071370; BAB85978.1; SEQUENCE 467 AA; 50964 M
                                                                                                                                               STRAIN-CV. MIDORIUSUI; TISSUE-DARK GROWN STEM;
                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                  Pisum sativum (Garden pea)
                                                                                                                                                                                                                                                                                       PSAPY2
                                                                                                                                                                                                                                                                                                                                                                      Q8RVT6;
                                                                                                                                                                                                                                                                                                                                                                                      Q8RVT6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Putative apyrase. OSJNBB0048D20.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8S7F1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8S7F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 KTVGVIDLGGASVQ 212
                                                                                                                                                                                                   NCBI_TaxID=3888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 DPHKTIGIIELGGASAQ 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 DTQETYGALDLGGASTQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 ETYGALDLGGASTQ 19
 9;
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                50964 MW; 94167066C46E0D3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 10; Length 635; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 48; DB 10; Length 462; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                    467 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         635 AA
 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,:
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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 0;
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Qy 3 DTQETYGALDLGGASTQ 19
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Db 210 DYSKTVGVVDLGGGSVQ 226
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Search completed: February 11, 2003, 18:39:40 Job time: 94 secs

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